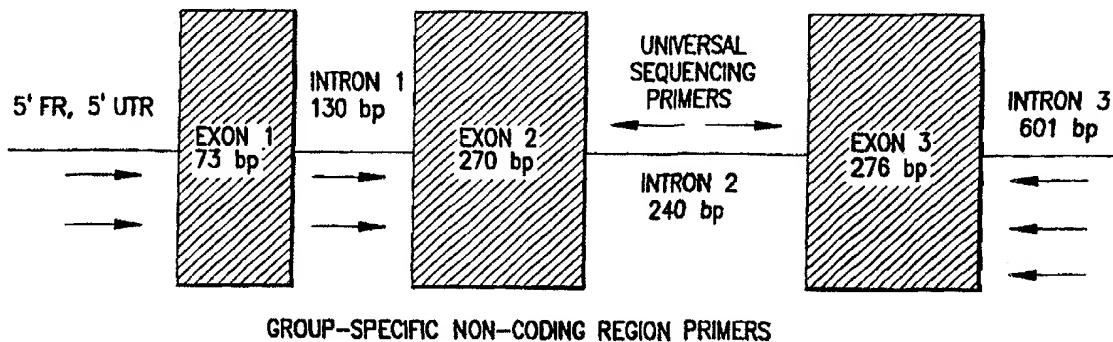




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(54) Title: METHOD AND KIT FOR HLA CLASS I TYPING



(57) Abstract

The present invention relates to methods and materials for determining the HLA Class I type of a subject, wherein group-specific sequences are used to design primer molecules which may be used in amplification protocols which accurately identify the HLA group(s) and/or allele(s) carried by the subject.

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Description

Method And Kit For HLA Class I Typing

1. Introduction

The present invention relates to methods and materials for determining the HLA Class I type of a subject, wherein group-specific sequences are used to design primer molecules which may be used in amplification protocols which accurately identify the HLA group(s) and/or allele(s) carried by the subject.

2. Background Of The Invention

The Histocompatibility Locus Antigen ("HLA") Class I genes comprise three classical genes encoding the major transplantation antigens HLA-A, HLA-B, and HLA-C and seven other Class I genes of which HLA-E, HLA-F and HLA-G are probably functional genes and HLA-H, HLA-I, HLA-K and HLA-L are pseudogenes. The class I genes share a similar structure, which includes, *inter alia*, 5' -> 3', a 5' untranslated flanking region; a first exon ("exon 1") having a length of approximately 73 base pairs ("bp"); a first intron ("intron 1") having a length of approximately 130 bp; a second exon ("exon 2"), having a length of approximately 250 bp; a second intron ("intron 2"), having a length of approximately 272 bp; a third exon ("exon 3"), having a length of approximately 276 bp; a third intron ("intron 3"), having a length of approximately 588 bp; and a fourth exon ("exon 4").

The HLA Class I genes are highly polymorphic among individuals. As of 1996, at least 73 alleles of HLA-A, 126 alleles of HLA-B and 35 alleles of HLA-C have been identified. This variability is of particular relevance when tissue transplantation between a donor and a host is contemplated. The histocompatibility antigens of donor and host should be as similar as possible to avoid both immune rejection of the transplanted tissue as well as graft-versus-host disease. It is therefore important to accurately identify the HLA types of donor and host. In view of the exigencies implicit in tissue transplantation, it is desirable that the typing be accomplished as efficiently as possible.

Methods for determining alleles of HLA-A, HLA-B, and HLA-C in a

patient sample have been heavily investigated because of the functional importance of these genes in transplant tissue matching and autoimmune diseases. The first tests developed used immunological methods to identify epitopes expressed by various HLA loci. These tests (*e.g.*, the complement-dependent cytotoxicity assay described in Terasaki and McClelland, *Nature*, 204:998, (1964)) identified broad serological specificities but were not capable of distinguishing between allelic members of a group, and sometimes mis-identified groups altogether. Unfortunately, even the most accurate of such low resolution assays cannot detect and distinguish all functionally significant transplant antigens (Anasetti et al. *Hum. Immunol.*, 29:70 (1990)).

High resolution tests performed at the nucleic acid level which distinguish among alleles of each group have become the focus of recent research. Current methods of high resolution typing include the following.

The Sequence Specific Oligonucleotide Probes ("SSOP") technique, as described in United States Patent No. 5,451,512 assigned to Hoffman-La Roche, Inc., uses a reverse dot blot format, wherein HLA-A probes are immobilized on a membrane, and the labelled target (patient sample) DNA is hybridized to the membrane-bound probe (as described in Saiki et al., 1989, *Proc. Natl. Acad. Sci.* 86:6230-6234). The pattern of hybridization to the probes on the dot-blot gives information regarding the HLA type of the individual. However, because hybridization is inherently not sufficiently specific to rule out minor differences in sequence between probe and patient sample, there is a possibility that the patient sample may contain an allelic variant which is not accounted for.

Another nucleic acid-based test is the Amplification Refractory Mutation System (ARMS) as described in the "HLA Class I SSP ARMS-PCR Typing Kit" Reference Manual, June 1995 edition, published by the Imperial Cancer Research Fund. This assay is based on the need for complementarity (matching) between the 3' end of an amplification primer and a target DNA sequence. Absent such matching, the primer will not function properly and no fragment will be amplified. Sequence information is deduced by determining, for various pairs of primers acting on target DNA from a patient sample, whether or not a fragment is successfully amplified. The accuracy of the technique is limited by the number of

primer pairs tested and by the possibility that allelic variations exist in regions of DNA which lie between the primers.

In order to overcome the foregoing shortcomings, it has been proposed that typing be accomplished by direct DNA sequencing (Santamaria et al., "HLA Class I Sequence-Based Typing" *Hum. Immunol.* 37, 39-50 (1993); WO 9219771; US Pat. 5,424,184). However, while direct sequencing of a patient's Class I HLA locus may conceptually be the most accurate, such sequencing may require a time-frame unsuitable for clinical practice. The success of direct sequencing methods may be expected to rely upon the design of efficient protocols and relevant primer sequences.

Prior to the present invention, direct sequencing protocols have exhibited a number of disadvantages. For example, the method of Santamaria et al., *supra*, fails to provide sufficient information because it focuses on cDNA (exon) sequences which, in view of exon sequence diversity, offer a very limited selection of conserved primer hybridization sites. In addition, because the Santamaria sequencing primers hybridize within an exon, they do not provide information for DNA sequence upstream of the primer which is potentially decisive for distinguishing among alleles. Further, the sites disclosed were determined before the recent discovery of dozens of more alleles that now need to be considered in identifying HLA type.

Intron sequences could provide the preferred hybridization sites for amplification and sequencing primers for the HLA-A, HLA-B and HLA-C genes because they may provide the DNA sequence of the full exon. Intron sequences for an HLA Class I gene were disclosed at least as early as 1985 (Weiss et al *Immunobiol* 170:367-380, (1985)). Due to their substantial diversity, and the difficulties in sequencing, few intron sequences have been published subsequently.

A number of researchers have made limited use of intron based oligonucleotides for limited aspects of HLA Class I typing.

Blasczyk et al. (*Tissue Antigens* 1996: 47: 102-110) used exon based amplification primers to determine group specificity. After amplification, universal sequencing primers located in intron 2 were used to sequence the amplified fragment. The paper does not disclose any intron sequence motifs from intron 1 or 3 or the 5'

untranslated region.

Cereb et al. (Tissue Antigens 1995: 45:1-11), undertook the identification of intron sequences useful for locus-specific amplification primer sets for all Class I genes. These primer sets were designed to amplify all alleles of the same locus. No group specific amplification primers were sought or reported. Further, amplified fragments were characterized by SSOP and not by direct sequencing.

Johnston-Dow et al (Poster Presentation: 1995 ASHI Meeting, Dallas, TX) presented a system for direct sequence determination of HLA-A wherein degenerate exon based primers were used to amplify exons 1 to 5 of the genomic HLA-A DNA sequence. As in Cereb et al., supra, the degenerate primer pool was designed to amplify all alleles of the HLA-A locus. Group specificity was not sought or reported. Further, sequencing of the amplified fragment was obtained using a degenerate primer mix wherein primers hybridize to intron regions flanking exons 2 and 3.

A rational approach to typing of classical HLA Class I loci would provide a simplified series of steps for high resolution typing of each allele of each loci in a patient sample using intron based oligonucleotides. Further, this method would be able to identify new alleles without ambiguities.

3. Summary Of The Invention

The present invention relates to materials and methods for high-resolution, nucleic acid-based typing of the three classical HLA Class I genes (comprising the loci HLA-A, HLA-B and HLA-C) in a patient sample. It is based, in part, on the discovery of group-specific sequence motifs, derived from the analysis of numerous patient samples, which include sequences of the 5' flanking region, intron 1, intron 2, and intron 3. Such sequence motifs may be used to design amplification primers which may be used to identify the HLA group or type of a subject. The invention is also based, in part, on the determination of numerous allele-specific sequences which may be used to confirm the precise allelic type of a subject.

The present invention provides for substantially purified nucleic acids which are capable of selectively hybridizing with group specific sequence motifs in untranslated regions of the HLA-A, HLA-B or HLA-C gene loci. Such nucleic acids, which may be comprised in a kit, may be used, alone or in conjunction with exon-based primers, to determine the group specificity of HLA-A, HLA-B, or HLA-C alleles contained in a patient sample and to identify the specific alleles present.

In particular embodiments, the present invention provides for methods of ascertaining the HLA Class I type of a subject which comprise performing a first amplification reaction which identifies the group type of the subject, and a second amplification reaction which produces allele-specific nucleic acids for sequencing.

3.1. Definitions

"Allele" means one of the alternative forms of the gene in question;

"Amplification" means the process of increasing the relative abundance of one or more specific genes or gene fragments in a reaction mixture with respect to the other genes. A method of amplification which is well known by those skilled in the art is the polymerase chain reaction (PCR) as described in United States Patents Nos. 4,683,194, 4,683,195 and 4,683,202, which are incorporated herein by reference. The PCR process involves the use of pairs of primers, one for each complementary strand of the duplex DNA (wherein the coding strand is referred to as the "sense strand" and its complementary strand is referred to as the "antisense strand"), that will hybridize at a site located near a region of interest in a gene. Chain

extension polymerization (without a chain terminating nucleotide) is then carried out in repetitive cycles to increase the number of copies of the region of interest many times. The amplified oligonucleotides are then separated from the reaction mixture and used as the starting sample for the sequencing reaction. Gelfand et al. have described a thermostable enzyme, "Taq polymerase," derived from the organism *Thermus aquaticus*, which is useful in this amplification process (see United States Patent Nos. 5,352,600 and 5,079,352 which are incorporated herein by reference);

"Group" as used herein, refers to a subset of alleles of one loci, all of which share sequence features which distinguish them from other groups. For example, serological group reactivity (in a lymphocytotoxicity assay) is the conventional basis for nomenclature of HLA alleles. The first two digits of an allele refer to the serological group; for example, the designation A*0201, A*0202, A*0217 all are members of the A2 group. Further, typically the nomenclature refers to the serological split group (e.g., A23 and A24 are serological splits of A9;

"Group-specific sequence motif" means a generally short, 1-25 nucleotide ("nt") sequence of nucleic acid which is found only in one or a few groups. Where a motif is shared by several groups in one region of the HLA locus, group-specific sequence motifs in other regions of the locus may serve as group-distinguishing features. The motif may share one or more nucleotides with the consensus sequence for the region;

"Haplotype" means the allele present on one chromosome;

"Heterozygote" means the presence of at least two different alleles of a gene;

"Homozygote" means the presence of a single species of allele of a gene;

"Locus" means a gene, such as HLA-A, HLA-B or HLA-C;

"Locus specific" means an event or thing associated with only one locus;

"Patient sample" means a sample collected from a patient in need of HLA typing which contains a sufficient amount and quality of nucleic acid (preferably DNA) for the performance of an amplification reaction. A nonlimiting example of a suitable source is peripheral blood lymphocytes, tissue (including cell

cultures derived therefrom, mucosal scrapes, spleen and bone marrow;

"Primer" means a polynucleotide generally of 5-50 nucleotides length which can serve to initiate a chain extension reaction;

"Sequencing" or "DNA sequencing" means the determination of the order of nucleotides in at least a part of a gene. A well known method of sequencing is the "chain termination" method first described by Sanger et al., Proc. Nat'l Acad. Sci. (USA) 74(12): 5463-5467 (1977) (recently elaborated in EP-B1- 655506, and Sequenase 2.0 product literature (Amersham Life Sciences, Cleveland) incorporated herein by reference). Basically, in this process, DNA to be sequenced is isolated, rendered single stranded, and placed into four vessels. In each vessel are the necessary components to replicate the DNA strand, which include a template-dependant DNA polymerase, a short primer molecule complementary to a known region of the DNA to be sequenced, and individual nucleotide triphosphates in a buffer conducive to hybridization between the primer and the DNA to be sequenced and chain extension of the hybridized primer. In addition, each vessel contains a small quantity of one type of optionally detectably labeled dideoxynucleotide triphosphate, *e.g.*, dideoxyadenosine triphosphate ("ddA"), dideoxyguanosine triphosphate ("ddG"), dideoxycytosine triphosphate ("ddC"), or dideoxythymidine triphosphate ("ddT"). In each vessel, each piece of the isolated DNA is hybridized with a primer. The primers are then extended, one base at a time to form a new nucleic acid polymer complementary to the isolated pieces of DNA. When a dideoxynucleotide is incorporated into the extending polymer, this terminates the polymer strand and prevents it from being further extended. Accordingly, in each vessel, a set of extended polymers of specific lengths are formed which are indicative of the positions of the nucleotide corresponding to the dideoxynucleic acid in that vessel. These sets of polymers are then evaluated using gel electrophoresis to determine the sequence.

"Specific hybridization" means hybridization of one strand of a nucleic acid to its complement.

"Target sequence" means the preferred site for specific hybridization of a primer; and

"Untranslated region" refers to a portion of an HLA locus which is not transcribed into RNA and eventually translated into protein. Examples of untranslated regions are the 5' and 3' flanking regions and intron sequences. For example, the 5' flanking region is neither transcribed nor translated, and intron sequences are transcribed but not translated.

4. Description Of The Figures

FIGURE 1 is an illustration of the principle for an HLA class I sequencing strategy. Group-specific primers are used for PCR amplification, and universal primers located in the 2nd intron are used for sequencing, regardless of the amplified group. 5'FR= 5' flanking region; 5' UTR= 5' untranslated region (-1 to -23 from the ATG start codon in exon 1).

FIGURE 2A and 2B depict, in schematic form, a method of the invention in which a cocktail of HLA-A group specific primers is used to amplify target DNA contained in a patient sample. The products of amplification are then separated electrophoretically in an agarose gel, allowing the identification, by fragment mobility, of fragments corresponding to groups A2 and A3. Primers specific for groups A2 and A3 are then used to amplify duplicate samples of target DNA in separate reactions, to produce A2 and A3 fragments which may then be sequenced using universal sequencing primers. FIGURE 2C and 2D depict a strategy wherein group type specificity is determined by reaction of aliquots of genomic DNA in separate reactions with a panel of primer pairs.

FIGURE 3 depicts the nucleic acid sequences of the HLA-A 5' flanking region in various alleles, including a consensus sequence (SEQ ID NO:1) as well as the sequences for the following alleles: A*0101 (SEQ ID NO:2); A*0301 (SEQ ID NO:3); A*1101 (SEQ ID NO:4); A*1102 (SEQ ID NO:5); A*3001 (SEQ ID NO:6); A*3002 (SEQ ID NO:7); A*3004 (SEQ ID NO:8); A*0201-11 (SEQ ID NO:9); A*0215 (SEQ ID NO:10); A*0217 (SEQ ID NO:11); A*6801 (SEQ ID NO:12); A*6802 (SEQ ID NO:13); A*6901 (SEQ ID NO:14); A*2301 (SEQ ID NO:15); A*2402 (SEQ ID NO:16); A*2403 (SEQ ID NO:17); A*2404 (SEQ ID NO:18); A*2405 (SEQ ID NO:19); A*2407 (SEQ ID NO:20); A*2501 (SEQ ID NO:21); A*2601 (SEQ ID NO:22); A*3402 (SEQ ID NO:23); A*4301 (SEQ ID

NO:24); A*6601 (SEQ ID NO:25); A*6602 (SEQ ID NO:26); A*6603 (SEQ ID NO:27); A*2901 (SEQ ID NO:28); A*2902 (SEQ ID NO:29); A*31012 (SEQ ID NO:30); A*3201 (SEQ ID NO:31); A*3301 (SEQ ID NO:32); A*3303 (SEQ ID NO:33); A*7401 (SEQ ID NO:34); A*7402 (SEQ ID NO:36); A*7403 (SEQ ID NO:37); and A*8001 (SEQ ID NO:38).

FIGURE 4 depicts the nucleic acid sequences of HLA-A intron 1 in various alleles, including a consensus sequence (SEQ ID NO:39) as well as the sequences for the following alleles: A*0101 (SEQ ID NO:40); A*0301 (SEQ ID NO:41); A*1101 (SEQ ID NO:42); A*1102 (SEQ ID NO:43); A*3001 (SEQ ID NO:44); A*3002 (SEQ ID NO:45); A*3004 (SEQ ID NO:46); A*0201 (SEQ ID NO:47); A*0202 (SEQ ID NO:44); A*0203 (SEQ ID NO:49); A*0204 (SEQ ID NO:50); A*0205 (SEQ ID NO:51); A*0206 (SEQ ID NO:52); A*0207 (SEQ ID NO:53); A*0207 (SEQ ID NO:54); A*0208 (SEQ ID NO:55); A*0209 (SEQ ID NO:56); A*0210 (SEQ ID NO:57); A*0211 (SEQ ID NO:58); A*0215 (SEQ ID NO:59); A*0217 (SEQ ID NO:60); A*6801 (SEQ ID NO:61); A*6802 (SEQ ID NO:62); A*6901 (SEQ ID NO:63); A*2301 (SEQ ID NO:64); A*2402 (SEQ ID NO:65); A*2403 (SEQ ID NO:66); A*2404 (SEQ ID NO:67); A*2405 (SEQ ID NO:68); A*2407 (SEQ ID NO:69); A*2501 (SEQ ID NO:70); A*2601 (SEQ ID NO:71); A*3402 (SEQ ID NO:72); A*6601 (SEQ ID NO:73); A*6602 (SEQ ID NO:74); A*6603 (SEQ ID NO:75); A*4301 (SEQ ID NO:76); A*2901 (SEQ ID NO:77); A*2902 (SEQ ID NO:78); A*3101 (SEQ ID NO:79); A*3201 (SEQ ID NO:80); A*3301 (SEQ ID NO:81); A*3303 (SEQ ID NO:82); A*7401 (SEQ ID NO:83); A*7402 (SEQ ID NO:84); A*7403 (SEQ ID NO:85); and A*8001 (SEQ ID NO:86).

FIGURE 5 depicts the nucleic acid sequences of HLA-A intron 2 in various alleles, including a consensus sequence (SEQ ID NO:87) as well as sequences for the following alleles: A*0101 (SEQ ID NO:88); A*0201 (SEQ ID NO:89); A*0202 (SEQ ID NO:90); A*0203 (SEQ ID NO:91); A*0204 (SEQ ID NO:92); A*0205 (SEQ ID NO:93); A*0206 (SEQ ID NO:94); A*0207 (SEQ ID NO:95); A*0208 (SEQ ID NO:96); A*0209 (SEQ ID NO:97); A*0210 (SEQ ID NO:98); A*0211 (SEQ ID NO:99); A*0215 (SEQ ID NO:100); A*0217 (SEQ ID NO:101);

A*6801 (SEQ ID NO:102); A*6802 (SEQ ID NO:103); A*6901 (SEQ ID NO:104); A*2501 (SEQ ID NO:105); A*2601 (SEQ ID NO:106); A*4301 (SEQ ID NO:107); A*6601 (SEQ ID NO:108); A*6602 (SEQ ID NO:109); A*6603 (SEQ ID NO:110); A*3402 (SEQ ID NO:111); A*2901 (SEQ ID NO:112); A*2902 (SEQ ID NO:113); A*3101 (SEQ ID NO:114); A*3201 (SEQ ID NO:115); A*3301 (SEQ ID NO:116); A*3303 (SEQ ID NO:117); A*7401 (SEQ ID NO:118); A*7402 (SEQ ID NO:119); A*7403 (SEQ ID NO:120); A*2301 (SEQ ID NO:121); A*2402 (SEQ ID NO:122); A*2403 (SEQ ID NO:123); A*2404 (SEQ ID NO:124); A*2405 (SEQ ID NO:125); A*2407 (SEQ ID NO:126); A*0301 (SEQ ID NO:127); A*1101 (SEQ ID NO:128); A*1102 (SEQ ID NO:129); A*3001 (SEQ ID NO:130); A*3002 (SEQ ID NO:131); A*3004 (SEQ ID NO:132); and A*8001 (SEQ ID NO:133).

FIGURE 6 depicts the nucleic acid sequences of HLA-A intron 3 in various alleles, including a consensus sequence (SEQ ID NO:134) as well as sequences for the following alleles: A*0101 (SEQ ID NO:135); A*0301 (SEQ ID NO:136); A*1101 (SEQ ID NO:137); A*1102 (SEQ ID NO:138); A*3001 (SEQ ID NO:139); A*3002 (SEQ ID NO:140); A*3004 (SEQ ID NO:141); A*0201 (SEQ ID NO:142); A*0202 (SEQ ID NO:143); A*0203 (SEQ ID NO:144); A*0204 (SEQ ID NO:145); A*0205 (SEQ ID NO:146); A*0206 (SEQ ID NO:147); A*0207 (SEQ ID NO:148); A*0208 (SEQ ID NO:149); A*0209 (SEQ ID NO:150); A*0210 (SEQ ID NO:151); A*0211 (SEQ ID NO:152); A*0215 (SEQ ID NO:153); A*0217 (SEQ ID NO:154); A*6801 (SEQ ID NO:155); A*6802 (SEQ ID NO:156); A*6901 (SEQ ID NO:157); A*2301 (SEQ ID NO:158); A*2402 (SEQ ID NO:159); A*2403 (SEQ ID NO:160); A*2404 (SEQ ID NO:161); A*2405 (SEQ ID NO:162); A*2407 (SEQ ID NO:163); A*2501 (SEQ ID NO:164); A*2601 (SEQ ID NO:165); A*3402 (SEQ ID NO:166); A*4301 (SEQ ID NO:167); A*6601 (SEQ ID NO:168); A*6602 (SEQ ID NO:169); A*6603 (SEQ ID NO:170); A*2901 (SEQ ID NO:171); A*2902 (SEQ ID NO:172); A*3101 (SEQ ID NO:173); A*3201 (SEQ ID NO:174); A*3301 (SEQ ID NO:175); A*3303 (SEQ ID NO:176); A*7401 (SEQ ID NO:177); A*7402 (SEQ ID NO:178); A*7403 (SEQ ID NO:179); and A*8001 (SEQ ID NO:180).

FIGURE 7 depicts a phylogenetic tree of the 5' flanking and 5' untranslated regions of HLA-A.

FIGURE 8 depicts a phylogenetic tree of introns 1-3 of the HLA-A gene.

FIGURE 9 depicts a phylogenetic tree of introns 1-3 of the HLA-B gene.

FIGURE 10 depicts the results of amplification using group-specific exon region primers to determine HLA-A group type, wherein the group specificity is determined to be 6601 and 3201 (see Table 7).

FIGURE 11 depicts the results of amplification using group-specific exon region primers to determine HLA-A group type, wherein the group specificity is determined to be 020x and 680x (see Table 8).

5. Detailed Description Of The Invention

The present invention relates to compositions and methods which may be used to efficiently and accurately determine the HLA Class I type of a patient sample.

The present invention is based, in part, on the determination of group-specific sequence motifs in regions of HLA Class I loci. These motifs may be used to design oligonucleotides which may be used as group-specific primers in nucleic acid amplification reactions. The present invention is also based, in part, on the determination of the sequences of regions of a wide variety of alleles of HLA Class I loci; such sequences may be used to distinguish one allele from another. Sequences of regions including the 5' flanking region of HLA-A and introns 1, 2 and 3 of HLA-A are provided herein, and are set forth in Figures 3-6.

In general, the methods of the invention may be described as follows. Comparison of nucleotide sequences of an HLA locus among members of an HLA Class I group, which lie in either untranslated or exon regions, may be used to identify group-specific motif sequences. Identification of groups may be by establishing serological relationships or using phylogenetic information, as set forth in Figures 7-9. Based on the group-specific motif sequences, oligonucleotide primers may be designed, synthesized, and used to amplify a portion of the HLA locus.

Oligonucleotides used in this manner are referred to herein as "group-specific

primers" and, in particular, as "group-specific untranslated region primers" or "group-specific exon region primers", as the case may be.

In preferred nonlimiting embodiments of the invention, the primers correspond to untranslated regions of the HLA Class I locus ("group-specific untranslated region primers"). Such primers may be used in pairs, wherein each member of the pair hybridizes to an untranslated region lying on either side of at least one exon. For example, but not by way of limitation, primer pairs may be oligonucleotide pairs which hybridize to group-specific motifs in the 5' untranslated region and the first, second, or third intron; the first intron and the second or third intron; or the second and third intron.

The group-specific primers may be used in several different methods according to the invention. In a first series of nonlimiting embodiments, the group-specific primers may be used in a diagnostic manner to identify which allelic groups are present in a patient sample. In a second series of nonlimiting embodiments, the group-specific primers may be used to amplify sufficient amounts of a particular allelic fragment which is then subjected to direct nucleotide sequencing using universal sequencing primers.

According to the first series of embodiments, the present invention provides for a method of determining the HLA Class I group type of a subject comprising (i) combining a group-specific primer pair with a target DNA sample from the subject under conditions such that primer-based amplification of the target DNA may occur; and (ii) determining whether a nucleic acid product is produced by the amplification; wherein the ability of a primer pair to produce a nucleic acid product is associated with a particular HLA group type. The group-specific primers may be group-specific exon region primers or group-specific untranslated region primers. In related embodiments the present invention provides for a method of determining the HLA Class I group type of a subject comprising (i) combining a plurality of group-specific exon region primer pairs with a target DNA sample from the subject under conditions such that primer-based amplification of the target DNA may occur; (ii) determining the size of the nucleic acid products of the amplification; and (iii) correlating the size of the product with the predicted size of a fragment associated

with a particular HLA group type. The plurality of primers is referred to as an HLA "cocktail" (see Figures 1 and 2). These first methods may be used to provide useful diagnostic information. For example, group type determination may serve as a first level of comparison for a histocompatibility analysis, even without identification of the specific allele(s) involved. For example, if a potential donor and host are being evaluated for tissue transplantation, if it is found that their group types do not match, no further comparison may be necessary. If, alternatively, their types do match, further analysis, for example by direct sequencing, may be desirable.

According to the second series of embodiments, the present invention provides for a method of determining the HLA Class I allelic type of a subject comprising (i) combining a group-specific oligonucleotide primer pair with a target DNA sample from the subject under conditions such that primer-based amplification of the target DNA may occur; (ii) collecting the nucleic acid product of the amplification; and (iii) determining the nucleic acid sequence of the product. The group-specific primer pair used may be determined based on the group type of the subject, as determined using the first method, described above. In preferred embodiments of the invention, group-specific untranslated region primers which span a region of the HLA locus containing allele-specific sequence may be utilized. If a subject is heterozygous, separate amplification reactions are performed for each group identified (e.g., separate reactions to amplify fragment for group A2 and group A3; see Figure 2). Sequencing may be performed using universal sequencing primers which will operate irrespective of HLA group or allelic type.

A more detailed description of the invention follows. Most alleles of the classical HLA Class I gene loci (consisting of HLA-A, HLA-B and HLA-C) can be distinguished on the basis of exon 2 and 3 alone. In one non-limiting embodiments, a method of the invention takes advantage of this fact, and employs the strategy generally described in Figure 2, using the example of HLA-A. A genomic DNA sample is prepared from a patient sample according to well known techniques. Aliquots of the genomic DNA may then separately be reacted with a panel of group-specific exon region primer pairs (Figure 2C), wherein the successful amplification of a DNA fragment is associated with a particular group type. Alternatively, as depicted

in Figure 2A), part of the sample may be treated with a cocktail of group-specific exon region primer pairs. Each primer pair in the cocktail will amplify only selected allelic groups because they specifically hybridize to group specific intron sequence motifs. Between them, under suitable polymerase chain reaction (PCR) conditions, the cocktail may amplify all known HLA-A groups, with each group specific amplification product having a different length. When reaction products are separated on an agarose gel the group(s) present in the patient sample may be identified by length.

Optionally, once the group specificity is determined, the direct sequence of alleles may be determined for precise allelic identification. As illustrated in Figure 2 B), a further part of the patient sample DNA may be treated under PCR conditions with a pair of primers that are specific for the previously determined group; preferably such primers are group-specific untranslated region primers, which span greater distances of the locus. If two groups were detected, then two separate reactions are performed. At completion of the second amplification, the reaction products are sequenced using an intron based "universal primer" which hybridizes to an intron sequence which is conserved among all alleles of the locus. Though it is theoretically possible to use a sequencing primer which is specific for the amplified group only, it is found that using a universal primer simplifies the method and the preparation of a kit. Various universal sequencing primers are specifically provided herein (see *infra*) which hybridize, respectively, to intron sequences flanking the 5' end of exon 2, the 3' end of exon 2, the 5' end of exon 3 and the 3' end of exon 3.

The substantial advantage of the method of the invention is that the initial group specific amplification allows a PCR based separation of haplotypes in 95% of patient samples. The separation of the haplotypes is a major achievement of this protocol since it permits the resolution of cis/trans linkages of heterozygote sequencing results which cannot be achieved with other protocols. With the instant invention, a separation of the haplotypes may be achieved in serological heterozygous samples with the sequencing primer mixes ("PMs") described in Table 2 (*infra*) using group-specific amplification corresponding to the serological families. The selection of the PMs used for sequencing depends on the amplification patterns of the preceding

PCR-SSP low-resolution typing. The primers are designed to work with a in a single cycle protocol including, but not limited to, a PCR protocol on a Perkin Elmer System 9600, maintaining typing capacities of the laboratory. All PCR products carry sufficient sequence information for a complete subtyping. This approach is superior to a typing system using a single pair of generic primers followed by direct sequencing or SSO hybridization, even if the amplification strategy is locus-specific. The substantial advantage of Sequence Based Typing (SBT) is the definition of the cis/trans linkage of sequence motifs. SBT after generic PCR amplification cannot define the cis/trans linkage of sequence motifs and therefore mimics oligotyping. The rapidly growing number of newly identified alleles confirms that new alleles have arisen mainly from gene conversion events which have usually taken place between different alleles of the same locus. Newly identified alleles are not characterized by new sequence motifs, but by a new combination of already existing sequence motifs. From this observation it may be concluded that the amount of alleles at each locus may theoretically represent all possible combinations of known sequence motifs. Of course, some of them will fall victim to negative selection. Nevertheless, it can be expected that still an enormous amount of alleles are yet unidentified. PCR-SSP subtyping strategies using a restricted number of oligonucleotides which do not cover all possible sequence motifs suffer from this limitation. If the cis/trans linkage of the analyzed polymorphic regions is not defined some new alleles may be mistyped as a heterozygous combination of known alleles. This has consequences with respect to SBT strategies. An unambiguous typing result of SBT after generic PCR amplification is only unambiguous with regard to the presently known HLA sequence databank. However, with the detection of new alleles this result can become ambiguous over the course of time. This observation has already been made in PCR based DRB1 typing during the last five years and will probably also occur in PCR based class I typing. Considering the above points, the idea of the instant SBT approach is not only to identify the HLA-A, HLA-B and HLA-C subtypes, but to cover as many of the polymorphic sites as possible and to define the cis/trans linkage of the polymorphic sequence motifs. Typing results obtained with this method will remain unambiguous independently of the growing HLA sequence databank.

In general, group-specific primers are desirably designed to facilitate hybridization to their intended targets. It should be taken into account that homology between different groups, and indeed between group-specific motifs, may exist. Accordingly, in preferred embodiments of the invention, a primer may be designed such that it hybridizes to its group target under relatively stringent conditions. For example, one or more mismatched residues may be engineered into the 3' domain of the molecule. Further, the primer may be designed such that it differs from any naturally occurring or consensus sequence, but rather has mismatches inserted which serve to further reduce hybridization of the primer to target DNA of a group other than the intended target group. Under certain circumstances, one or more mismatches may be introduced into the 5' end to destabilize internal hairpin loops; such changes are not generally expected to enhance the efficiency of the primer.

The following nucleic acid sequences may be comprised in group-specific untranslated region primers for HLA-A which are specific for the groups as indicated in Table 1.

Table 1.

<u>Designation</u>	<u>Sequence</u>	<u>N</u>	<u>Tm</u>	<u>Specificity</u>	<u>Position</u>
II-210m	S 5' ACC Cgg gAA gCC ggg CCT 3'	18	64 C	A10 et al.	73-92
II-230m	S 5' ggC Agg TCT CAg CgA Ctg 3'	18	60 C	A*01,03,11,30	102-119
II-226	S 5' CTC TgT ggg gAg AAg CAA C 3'	19	60 C	A*02	29-47
II-221m11	S 5' ggg AgC ggC gCC ggg AC 3'	17	64 C	A*0301	77-93
II-209	S 5' gAA gCA Agg ggC Ccg CCC	18	64 C	A10 et al.	41-58
II-214m	S 5' CgC CTg gCg ggg gGg CAA 3'	18	66 C	A*2301,24	54-71
II-223d	S 5' gTg AgT gCg ggg TCg Tgg 3'	18	62 C	A19	1-19
II-225m	S 5' gCC ggg Agg Agg gAC ggT 3'	18	64 C	A*30	86-103
II-237m14	S 5' ggC gCg CCC ggC ggg gA 3'	17	65 C	A*29	49-65
II-240	S 5' ggA ggA ggg Tcg ggC ggA 3'	18	64 C	A*31,33	90-107
5'FL-243	S 5' AgT gTC TTC gCg gTC gCT C 3'	19	62 C	A*11	53-71
5'FR-257	S 5' CTC AgA TTC TCC CCA gAC g 3'	19	60 C	Aall, except for A*11 6-24	
5'FR-273	S 5' CAT gCC gAg ggT TTC TCC CA 3'	20	64 C	A*28,6602,6603	360-380
BP202	S 5' CTg gCC CTg ACC CAg ACC A 3'	19	64 C	A*7401,7403	Exon 1, 49-68
BP203	S 5' CCT gAC CCA gAC CTg ggC A 3'	19	64 C	A*8001	Exon 1, 55-73
BP142	AS 5' C AGG TAT CTG CGG AGC CCG 3'	19	64 C	A*0101/**24	227-245
I3-236	AS 5' gTC TgT CAg gAA gAg TCA gAA 3'	21	62 C	A*non 02.28	584..+2
I3-239	AS 5' gTg gAA AAT TCT AgT CCC TgA A3'	22	62 C	A*multi,notA1,3,11,30.9	415-436
I3-246	AS 5' AgA TCT ACA ggC gAT CAg gA 3'	20	60 C	A*30	24-43
I3-247m6	AS 5' gCC AgC CCg ggA gTT CTA T 3'	19	62 C	A*01,11	36-54
I3-249	AS 5' CAg AgT CAC TCT CTg gTA Cag 21	62 C	All A,weak59,70,92, J,E,G,F		148-168
I3-280m18	AS 5' gCg ATC gTC TTC CCG TCA C 3'	19	62 C	A*01,03,11,30	221-239
I3-282	AS 5' AgA gTC ACT CTC Tgg TAC AgA 3'	21	62 C	A*8001	148-168

The sequences in Table 1 have the following sequence identifiers: II-210 is SEQ ID NO:35 and the remaining sequences II-230m through 13-282 have SEQ ID NO:181-202, respectively.

The present invention provides for nucleic acid molecules comprising regions having the foregoing sequences or their functional equivalents.

"Functional equivalents" of a nucleotide sequence, as defined herein, refers to nucleotide sequences which, when contained in a nucleic acid molecule, retain the specificity of the disclosed sequence and/or hybridize to the complement of the disclosed sequence under stringent hybridization conditions (e.g., .1 x SSC at 65°C).

In specific nonlimiting examples, oligonucleotides comprising the above sequences, or functional equivalents thereof which retain specificity, may be used in a PCR amplification reaction in the following pairwise combinations to generate group specific fragments of the lengths as indicated in Table 2.

Table 2.

No.	Primer Mix	Sense Primer	Antisense Primer	Size of Product	HLA-A Specificity
1	1.1	I1-230m	BP142	785 bp	A*01
2	1.2	5'FR-257	I3-247m6	1068 bp	A*01
3	1.3	I1-230m	I3-247mg	870 bp	A*01,11
4	2	I1-226	I3-249	1056 bp	A*02
5	3	I1-221m11	I3-280m18	1078 bp	A*03
6	11	5'FL-243	I3-249	1229 bp	A*11
7	9	I1-214m	I3-249	1033 bp	A*23,24
8	10.1	I1-210m	I3-236	1450 bp	A*10
9	10.2	I1-210m	I3-249	1014 bp	A*10,68,69
10	28	5'FR-273	I3-249	1537 bp	A*68,69, 6602,6603
11	19.1	I1-223d	I3-239 or I3- 249	1084 bp	A*29,31,32, 33,74
12	19.2	I1-240	I3-249	996 bp	A*31,33
13	29	I1-237m14	I3-249	1037 bp	A*29
14	30	I1-225m	I3-249	1000 bp	A*30
15	74	BP202 (Exon 1)	I3-249	1109 bp	A*7401, 7403
16	80	BP203	I3-282	1103 bp	A*8001 (untested)

The following nucleic acid sequences may be comprised in group-specific exon region primers for HLA-A which are specific for the groups as indicated in Table 3 (sense primers) and Table 4 (antisense primers). The present invention provides for nucleic acid molecules comprising regions having the foregoing sequences or their functional equivalents. They may, in specific nonlimiting examples, be used in pairs as set forth in Table 5. The sequences in Table 3, primer numbers 85, 118, 120, 123, 127, 129, 134, 137, 140, 160, 167, 175, 193 and 202 have SEQ ID NO:203-216, respectively. The sequences in Table 4, primer numbers 98, 115, 116, 117, 126, 133, 135, 136, 138, 142, 144, 145, 152, 153, 154, 155, 161, 165, 168 and 180, have SEQ ID NO:217-236, respectively, and primer number 119 has SEQ ID NO:245.

Table 3.

Primer Number	Localization	Sequence
85	Exon 2 -4 - 5	5' CTC CTC gTC CCC Agg CTC T 3'
118	Exon 2 6 - 19	5' TCC ATg Agg TAT TTC TAC ACC 3'
120	Exon 3 -6 - 12	5' ggC CAg gTT CTC AgA CCA 3'
123	Exon 2 36 - 53	5' CCC ggC CCg gCA gTg gA 3'
127	Exon 3 1 - 20	5' gTT CTC ACA CCA TCC AgA Tg 3'
129	Exon 3 4 - 25	5' TCA CAC CCT CCA gAT gAT gTT 3'
134	Exon 3 63 - 80	5' ggg TAC CAg CAg gAC gCT 3'
137	Exon 2 9 - 29	5' TCC ATg Agg TAT TTC ACC ACA 3'
140	Exon 3 -1 - 20	5' ggT TCT CAC ACC ATC CAg ATA 3'
160	Exon 3 1 - 20	5' gTT CTC ACA CCA TCC AgA gg 3'
167	Exon 2 54 - 71	5' gAg CCC CgC TTC AAC gCC 3'
175	Exon 3 63 - 71	5' CTT CCT CCg Cgg gTA TgA A 3'
193	Exon 2 167 - 184	5' gCC ggA gTA TTg ggA CCg 3'
202	Exon 1 49 - 67	5' CTg gCC CTg ACC CTg ACC A 3'

Table 4.

Antisense primers

Primer Number	Localization	Sequence
98	Exon 2 226 - 243	5' gCA ggg TCC CCA ggT CCA 3'
115	Exon 3 195 - 213	5' CCT CCA ggT Agg CTC TCA A 3'
116	Exon 3 195 - 213	5' CCT CCA ggT Agg CTC TCC A 3'
117	Exon 3 195-213	5' CCT CCA ggT Agg CTC TCT g 3'
119	Exon 2 184 - 203	5' CTT CAC ATT CCg TgT CTC CT 3'
126	Exon 3 212 - 230	5' CCA CTC CAC gCA CgT gCC A 3'
133	Exon 2 229 - 246	5' ggA gCg CgA TCC gcA ggC 3'
135	Exon 3 216 - 234	5' ggA gCC ACT CCA Cgg ACC g 3'
136	Exon 3 216 - 233	5' gAg CCA CTC CAC gCA CTC 3'
138	Exon 2 186 - 206	5' ggC CTT CAC ATT CCg TgT gTT 3'
142	Exon 3 228 - 246	5' CAg gTA TCT gCg gAg CCC g 3'
144	Exon 2 165 - 184	5' Tgg TCC CAA TAC TCA ggC CT 3'
145	Exon 2 226 - 243	5' gCA ggg TCC CCA ggT TCg 3'
152	Exon 3 163 - 179	5' ggg CCg CCT CCC AgT TgT 3'
153	Exon 2 179 - 197	5' TCT gTg AgT ggg CCT aCA CA 3'
154	Exon 2 184 - 204	5' CCT TCA CAT TCC gTg TCT gCA 3'
155	Exon 3 216 - 233	5' gAg CCA CTC CAC gCA CgT 3'
161	Exon 2 209 - 228	5' CCA CTC ggT CAg TCT CTg AC 3'
165	Exon 3 105 - 124	5' gAg CgCA ggT CCT CgT TCA A 3'
168	Exon 2 198 - 217	5' gTC TgT gAg Tgg gCC aTC AT 3'
180	Exon 2 12 - 31	5' CAg CCA TAC ATC CTC Agg AC 3'

Table 5.

Primer Mix No. Name		Sense Primer	Antisense Primer	Size of Product	HLA-A Specificity
1	1	140	142	247 bp	A*0101,0102,8001
2	2	85	98	256 bp	A*0201-0220
3	3	140	126	230 bp	A*0301,0302,0303
4	36	167	168	164 bp	A*0101,3601
5	11	118	119	195 bp	A*1101-1103
6	23	129	115	209 bp	A*2301
7	24	129	116+117	209 BP	A*2402-2411
8	10.1	160	135	233 bp	A*2501,2601- 2603,2605,4301,6601
9	25	118	133	238 bp	A*2501,2502
10	26	118	145	235 bp	A*2601,2602,2604,4301
11	34	134	155	171 bp	A*3401,3402
12	6602	134	136	240 bp	A*6602,6603
13	10.2	118	161	222 bp	A*11,34,6601,6602,68011, 6802,6901
14	43	118	154	196 bp	A*4301
15	68	120	152	185 bp	A*68011,68012,6802,6803
16	69	193	180	375 bp	A*6901
17	19	127	165	124 bp	A*2901,2902,31012,3201, 3301-3303, A*7401-7403
18	29	137	145	236 bp	A*2901,2902
19	30	175	115+116	162 bp	A*3001-3002
20	31	167	144	176 bp	A*31012
21	32	167	133	159 bp	A*3201,3202,2501,2502
22	33	137	138	198 bp	A*3301-3303
23	74	202	153	370 bp	A*7401,7403
24	80	140	136	234 bp	A*8001

In general, the foregoing group-specific primers may be modified by addition, deletion, or substitution of bases, to produce functionally equivalent primers with the substantially the same specificity, that is to say, such that the group specific polymorphism(s) are not removed. Such modifications may be constrained by several parameters. First, exact matching at the 3' end is particularly important for primer extension. Preferably, at least 5 nt are complementary to target DNA. When the exactly conserved region is short, for example, less than 10 nt, it is not advisable to change the primer sequences. The primer is preferably less than 50% G or C. Also, the primers should be designed to avoid specific hybridization with pseudogenes or non-classical HLA Class I loci. In the examples which follow, the melting temperature of all primers used was about 62C to ensure uniform amplification conditions.

For sequencing purposes, the following nucleic acid sequences are sequences which hybridize to all alleles of the indicated loci, in the locations indicated (and hence are referred to as universal sequencing primers).

Table 6:

Universal Sequencing Primers for HLA-A

Desig.	Sequence	Location	Melting Temp.
5'-Ex2(Aw3)	5' GCG CCG GGA GGA GGG TC 3'	Int-1	Tm=58-62°C
3'-Ex2	5' ATC TCG GAC CCG GAG ACT 3',	Int-2	Tm=58°C
5'-Ex3	5' GTT TCA TTT TCA GTT TAG GCC A 3'	Int-2	Tm=60°C
3'-Ex3(Aw6)	5' CGG GAG ATC TAC AGG CGA TCA GG 3'	Int-3	Tm=58-62°C
Desig.	Sequence	Location	Melting Temp.
5'-Ex2(Aw3)	5'GCG CCG GGA GGA GGG TC 3'	Int-1	Tm=58-62°C
3'-Ex2	5'GTC GTG ACC TGC GCC CC 3',	Int-2	Tm=58-62°C
5'-Ex3	5'GGG CGG GGC GGG GCT CGG G 3,	Int-2	Tm=58-62°C
3'-Ex3(Aw6)	5'CGG GAG ATC TAC AGG CGA TCA GG 3'	Int-3	Tm=58-62°C
Desig.	Sequence	Location	Melting Temp.
5'-Ex2(Aw3)	5' GCG CCG GGA GGA GGG TC 3'	Int-1	Tm=58-62°C
3'-Ex2(ABCw1)	5' GGT CGT GAC CT(T/C)CGC CCC 3'	Int-2	Tm=58-62°C
5'-Ex3(ABCw2)	5' CCC GGT TTC ATT TTC 3'	Int-2	Tm=58-62°C
3'-Ex3(Aw6)	5'CGG GAG ATC TAC AGG CGA TCA GG 3'	Int-3	Tm=58-62°C

The primers in Table 6 are assigned, consecutively, SEQ ID NO: 237-244.

The foregoing three groups of primers include 5' and 3' primers for sequencing across exons 2 and 3, respectively.

The selection of suitable universal sequencing primers is constrained by a variety of rules including the following. Sequencing primer hybridization sites must lie within the fragment amplified by the group specific amplification primers. All primers are desirably selected to provide informative sequence and not start too far downstream of useful sequence. Preferred primers hybridize to conserved sites near the exon/intron boundaries.

Direct sequencing of the 2nd and 3rd exon may be performed from either the 5' or 3' end using the primers of Table 6 *supra* which are located in conserved regions of the 1st, 2nd and 3rd intron as indicated. These conserved regions were found to be identical in all samples investigated, regardless of the amplified group.

An important issue of direct sequencing for HLA class I genes is the generation of a specific PCR product, which is rather complicated due to the

extensive sequence homologies between the different HLA class I loci including several pseudogenes. If an adequate PCR product has been generated, any sequencing chemistry should be applicable.

In the normal case, since group specific amplifications take place before sequencing, only one allele at a time is sequenced, resulting in unambiguous homozygous sequencing results. In these cases alleles are relatively easy to identify, even without software.

However, in about 5% of cases, both alleles come from the same group, but the sequence results show heterozygosity. In practice, when viewed by a fluorescence-detecting system, the sample appears as a normal sequence of bases with, sporadically, two bases at one site, each with half the peak height. This result flows from the high degree of similarity shared among all alleles of each HLA gene; sequence heterozygosity flows from base substitutions. The laborious task of determining which alleles are present in the test sequence may be simplified using computer analysis. A software program called GeneLibrarian developed by Visible Genetics, the assignee of the present application, rapidly compares the test sequence to a database which includes all possible homozygote and heterozygote combinations of the alleles. The program identifies those stored sequences that are closest matched to the test sequence. The operator can then determine which allelic pair is in the test sample. If no allelic pair shows an exact match, the software allows the operator to review the test sequence to determine if errors in base-calling or other artifacts are interfering with the analysis.

The order of sequencing reactions may be selected by the operator. Each exon of each locus may be sequenced on the sense strand or anti-sense strand. A preferred method is to obtain sequence from one strand from each exon. If the results contain ambiguities, then the amplicon is re-sequenced using the other primer for the same exon. The availability of both sequencing primers provides redundancy to ensure robust results.

In some cases, it may be advantageous to employ an equimolar mixture of 2 or more oligonucleotide species. Mixtures of oligonucleotides may be selected such that between them they will effectively prime the sequencing reactions for all

alleles of the locus at the same site.

In an alternative technique, instead of using dye terminators, a dye-labelled primer may be employed. In this case, the selected sequencing primers is labelled on the 5' end with a detectable label, using phosphoramidite or NHS/dye ester techniques well known in the art. The label selected depends on the detection instrument employed. The label for use with an OpenGene System (Visible Genetics Inc., Toronto, ON) is the fluorophore Cy5.5 (Amersham Life Sciences, Cleveland OH). Fluorescein-isothio-cyanate may be used for detection with the ALF Automated Sequencer (Pharmacia, Piscataway NJ). In this method, which is well known to one skilled in the art, the sequencing reaction mixture is changed slightly to include only one ddNTP per reaction mixture. For detection of reaction products, the sample may be mixed with an equal volume of loading buffer (5% ficoll plus a coloured dye). 1.5 μ l of these samples may be loaded per lane of a MicroCel electrophoresis cassette loaded in a MicroGene Blaster automated DNA sequencer (Visible Genetics Inc., Toronto). The sample may be electrophoresed and read.

Results may be displayed and analyzed with GeneObjects software. The sequence of bases may be determined, and the HLA allele to which the sequence corresponds may then be identified. This process may be performed for each locus (HLA-A, HLA-B, HLA-C) and the results may then be reported to the patient file.

It is well known in the art that different variations of sequencing chemistry may be employed with different automated DNA sequencing instruments. Single dye instruments, such as the OpenGene System (Visible Genetics Inc., Toronto), the ALF Express (Pharmacia, Uppsala, Sweden) or the Li-Cor 4000L (Lincoln City, Nebraska) generally use dye-labeled primers. In these systems a single chain termination sequencing reaction mixture is run per lane.

Multi-dye sequencers, such as the Prism 377 (applied Biosystems, Inc., Foster City, California) detect multiple dyes in a single lane. This technology conveniently employs dye-terminator chemistry, where the chain-terminating nucleotides are themselves labeled with fluorophores (see United States Patent No. 5,332,666, to Dupont de Nemours and Co.). In this case, the reaction products carrying four different labels may be run in a single lane.

Either single dye or multi-dye chemistry may be employed according to the present invention, along with other sequencing chemistries. Additional methods for reducing the numbers of reactions required to obtain detailed sequence information from the classical HLA Class I loci are disclosed in commonly owned United States Patent Applications USSN 08/577,858 (for single-track sequencing) and USSN 08/640,672 and 08/684,498 (for single-tube sequencing), incorporated by reference herein.

The nucleic acids described above may be comprised in a kit for use in practicing the methods of the invention. In addition to the group-specific primers and primer pairs disclosed, such kits may further comprise buffers, reagents, and enzymes such as, amplification enzymes including but not limited to, *Taq* polymerase. In specific, non-limiting embodiments, the kit may comprise group-specific exon region primers (for example, as a "cocktail" comprising a plurality of primers) as well as group-specific untranslated region primers; such primers may be contained in individual tubes.

6. Example: Determination Of HLA-A Group Type

Genomic DNA was prepared from patient samples according to standard methods, such as a standard salting-out procedure (as provided by the Puregene DNA Isolation Kit, Gentra Systems, Inc., Minneapolis) or by detergent and proteinase K treatment (Current Protocols in Molecular Biology, Eds. Ausubel, F.M. et al, (John Wiley & Sons; 1995)).

All primers were synthesized on a Gene Assembler plus (Pharmacia, Uppsala, Sweden), and purified by fast protein liquid chromatography. The sequence, length, melting temperature (Tm), group specificity localization of the primers are given in Tables 3 (sense primers), 4 (antisense primers) and 5 (primer pairs). Internal positive control primers were: 5' primer hGHI 5'GCC TTC CCA ACC ATT CCC TTA 3', 21mer, Tm=64°C, nucleotide position 5560-5580; 3' primer hGHI 5' TCC ATG TCC TTC CTG AAG CA 3', 20mer, Tm=60°C, nucleotide position 6614-6633. These control primers amplify a 1074 bp fragment of the human growth hormone gene.

Group-specific identification was performed as follows. Aliquots of

genomic DNA were separately reacted with a panel of 24 group-specific exon region primer pairs set forth in Table 5, *supra* (see Blasczyk et al., 1995, *Tissue Ant.* **46**:86-95). An amplification cocktail for pairs of primers was prepared in 10 μ l volume using standard 10x Perkin-Elmer buffer (1x buffer: 50 mM KCl; 1.5 mM MgCl₂; 10 mM Tris-HCl, pH 8.3; 0.001% (w/v) gelatin) supplemented with 5% glycerol and 0.1 μ l Cresol-red, sodium salt (Cresol-red stock solution:10 mg/ml). The use of glycerol and cresol red avoids the necessity of using an agarose gel loading buffer.

Additionally, glycerol increases the PCR yield.

The PCR mix for a single SSP tube was as follows:

Genomic DNA 100 ng	=	1.00 μ l
<i>Taq</i> polymerase, 0.4 U	=	0.08 μ l
dNTPs, 10 mM	=	0.80 μ l
Buffer, 10x	=	1.00 μ l
Glycerol	=	0.50 μ l
Cresol red 10mg/ml	=	0.10 μ l
dH ₂ O	=	1.52 μ l
Primer Pair + Control		
Primer Pair	=	<u>5.00 μl</u>
Total		10.00 μ l

The PCR solution was prepared in volumes that would accommodate 30 reactions. The amount of primers used in each 10 μ l PCR volume was 3 pmol of each HLA-A primer and 0.8 pmol of each internal control primer.

The reaction mixture was mixed well, then heated in a Thermo-Cycler 9600 (Perkin-Elmer, Inc) and subjected to the following protocol. After an initial denaturation, a first round with 10 two-temperature cycles was followed by 20 three-temperature cycles.

- 1) Initial denaturation at 95°C for 5 min.
- 2) First 10 cycles
 - i) Denaturation at 95°C for 30 sec.
 - ii) Annealing and extension at 65°C for 50 sec.
- 3) Last 20 cycles
 - i) Denaturation at 95°C for 30 sec.
 - ii) Annealing at 62°C for 50 sec.
 - iii) Extension at 72°C for 30 sec.

The reaction tube was then cooled on ice. For visualization, 8 ul of the amplification product were run on a 2 % agarose gel prestained with ethidium bromide (0.2 ug/ml). The results were compared to a control lane with known size markers. The reaction products were visualized either as two bands (alleles from different groups) or a single band (alleles from same group). The size of the band(s) were determined and group specificity was assigned according to the length assignments in Table 5.

Figures 10 and 11 show typical gel results, which, as shown in Tables 10 and 11, were interpreted to determine what group specificities were present in genomic DNA samples tested. In Tables 7 and 8, the column titled "Position" refers to the primer mix no. of Table 5.

Table 7.

<u>Position</u>	<u>HLA Specificity</u>	<u>Kontr.</u>	<u>Species ampl.</u>	<u>PM</u>
1	A*0101,0102,8001			1
2	A*0201-0217			2
3	A*0301,0302			3
4	A*0101,3601			36
5	A*1101,1102			11
6	A*2301			23
7	A*2402-2407			24
8	A*2603,2605,6601	X		10.1
9	A*2501			25
10	A*2601,2602,2604,4301			26
11	A*3401,3402			34
12	A*6602			6602
13	A*1101,1102,3401,3402, 6601,6602, A*68011,6802,6901	X		10.2
14	A*4301			43
15	A*68012,6802,6803			68
16	A*6901			69
17	A*2901,2902,3101,3201 3301-3303, A*7401	X		19
18	A*2901,2902			29
19	A*3001-3004			30
20	A*3101			31
21	A*3201,2501	X		32

Table 8.

<u>Position</u>	<u>HLA Specificity</u>	<u>Kontr.</u>	<u>Species</u>	<u>Ampl.</u>	<u>PM</u>
1	A*0101,0102,8001				1
2	A*0201-0217	X			2
3	A*0301,0302				3
4	A*0101,3601				36
5	A*1101,1102				11
6	A*2301				23
7	A*2402-2407				24
8	A*2501,2601-2603, 2605,6601				10.1
	A*2501				25
10	A*2601,2602,2604,4301				26
11	A*3401,3402				34
12	A*6602				6602
13	A*1101,1102,3401,3402 6601,6602, A*68011,6802, 6901	X			10.2
14	A*4301				43
15	A*6801,6802	X			68
16	A*6901				69
17	A*2901-2902,3101,3201, 3301-3303, A*7401				19
18	A*2901,2902				29
19	A*3001-3004				30

7. Example: Determination Of Group Specificity Using
A Primer Cocktail

Group specific low-resolution typing of the patient sample may be performed as follows. First, a stock PCR amplification reaction mixture may be prepared for 30 reactions:

	μ l
dNTPs 10mM	24
Glycerol 100%	15
10x PCR Buffer*	30
Cresol-red (10mg/ml)	3.0
H ₂ O	<u>45</u>
final	117

*1 X PCR Buffer comprises 10 MM Tris-HCl pH 8.3, 50 mM KCl, 1.5 mM MgCl₂ and 0.001% (w/v) gelatin.

The stock mixture may be prepared in a large volume and be stored for at least one month at 4°C or be aliquoted (117.0 μ l) and stored at -30°C for at least six months. Repeated thawing and freezing should be avoided.

A mixture containing all the HLA-A group specific amplification primers listed in Table 5 may be prepared separately (the "Cocktail"). One member of each primer pair is labelled on the 5' end with a fluorescent label. Final Cocktail concentrations may be designed to provide 3 pmol of each HLA-A primer per 5 μ l. Optionally, an internal control primer may be added (to determine among other things, the success of amplification) in the amount of 0.8 pmol per 5 μ l. Suitable internal control primers amplify a 1074 bp fragment of the human growth hormone gene (see *supra*).

To perform the low resolution amplification reaction, the reaction mixture may be prepared as follows:

	Volume
Stock Mixture	5 μ l
Cocktail	5 μ l
Patient sample DNA 100-250 ng	1 μ l
Taq Polymerase Enzyme 0.4 U	0.08 μ l

PCR cycle parameters may be adjusted for a Perkin-Elmer System 9600 thermal cycler. After an initial denaturation, a first round with 10 two-temperature cycles may be followed by 20 three-temperature cycles: 1) Initial Denaturation at 95°C for 5 min; 2) First 10 cycles i) Denaturation at 95°C for 30 seconds and ii) Annealing and extension at 65°C for 50 seconds; 3) Last 20 cycles i) Denaturation at 95°C for 30 seconds, ii) Annealing at 62°C for 50 seconds and iii) Extension at 72°C for 30 seconds.

The reaction tube may then be cooled on ice. For visualization, 2ul of the amplification product may be run on a polyacrylamide gel giving single nucleotide length resolution such as in a MicroGene Blaster. The results were compared to a control lane with known size markers. The reaction products may be visualized either as two bands (alleles from different groups) or a single band (alleles from same group). The size of the band(s) may be determined and group specificity may be assigned according to the length assignments in Table 5.

8. Example: Determination Of Allelic Type By Sequencing

After determining group type specificity, group specific amplification of a fresh portion of the patient sample may be performed using a single pair of primers specific for the group in question to generate sequencing template. In a preferred, nonlimiting embodiment, amplification primers may be selected from Table 2, *supra*, which lists group-specific untranslated region primers. This second amplification serves two purposes. First, it confirms, by successful amplification, the group determination of the low resolution test. Second, it generates sequence information which may be used for accurate allele identification. If two groups are identified, two separate reactions may be performed each using a different primer pair.

8.1. PCR Protocol

The same PCR protocol may be used for all primer mixes used for template generation. The PCR amplification may be set up in a total volume of 50 μ l in order to produce enough PCR product for more than 10 sequencing reactions. This ensures that, if anything fails during the sequencing process, sequencing can be repeated without generation of a new template. The high stringency of the PCR primers and protocol detailed below makes the use of a "hot start approach" unnecessary. The following PCR reaction mix may be used:

	<u>volume per reaction</u>
5X PCR buffer*	10.0 μ l
DMSO	1.0 μ l
2.5mM each dNTP	5.0 μ l
ddH ₂ O	<u>27.8μl</u>
Total	43.8 μ l
 Sense primer** (10pmol/ μ l)	1.0 μ l
Antisense primer** (10pmol/ μ l)	1.0 μ l
<i>Taq</i> Polymerase (5U/ μ l)	0.2 μ l
Genomic DNA (100ng/ μ l)	<u>4.0μl</u>
Final Total	50.0 μ l

*Composition of 5X PCR buffer: 75mM (NH₄)₂SO₄; 17.5mM MgCl₂; and 300mM Tris-HCl, pH 9.0

**The pair of group specific amplification primers may be selected from those disclosed in Table 2, *supra*.

PCR cycle parameters may be adjusted for a Perkin-Elmer System 9600 thermal cycler. After an initial denaturation, a first round with 10 two-temperature cycles may be followed by 20 three-temperature cycles.

- 1.) Initial Denaturation at 95 C for 5 min
- 2.) **First 10 cycles**
 - i) Denaturation at 95 C for 30 seconds
 - ii) Annealing and extension at 65 C for 50 seconds
- 3.) **Last 20 cycles**
 - i) Denaturation at 95 C for 30 seconds
 - ii) Annealing at 62 C for 50 seconds
 - iii) Extension at 72 C for 30 seconds

10 μ l of the PCR product may then be run on a 2 % agarose gel prestained with ethidium bromide (0.2 μ g/ml). A distinct band of the expected size should be seen.

8.2. Sequencing Reaction Protocol

The sequencing reactions may be carried out with AmpliTaqTM DNA Polymerase FS dye terminator cycle sequencing chemistry using the Ready Reaction DyeDeoxy Terminator Cycle Sequencing Kit FS (Perkin Elmer Applied Biosystems

Division, Foster City, CA) according to the manufacturer's protocol. This Kit contains the four ddNTPs with different fluorescence labels (=Dye Terminators). The PCR fragments may be used directly for sequencing without any prior purification step.

To simplify the pipetting steps, a master mix may be prepared consisting of the 5'Biotin labeled sequencing primer, ddH₂O and the Kit reagents. This master mix should be prepared immediately prior to use and can be kept at room temperature until use. The sequencing master mix for one reaction may comprise 3.0 μ l of a 1pmol/ μ l solution of sequencing primer; 6.0 μ l ddH₂O, and 8.0 μ l of premixed sequencing reagents; for 36 + 1 reactions, these amounts are increased, respectively, to 111.0 μ l; 222.0 μ l; and 296.0 μ l, respectively. The sequencing primer may be selected from the sequencing primers for HLA-A set forth in Table 6, *supra*:

The master mix may be aliquoted in a volume of 17 μ l for each sequencing reaction in a 200 μ l PCR tube and 3 μ l of the unpurified PCR product are added. The reaction mixes may then be subjected to 25 cycles in a Perkin Elmer thermal cycler 9600. Each cycle consists of 10 sec 95 C, 5 sec 50 C and 4 min 60 C.

8.3. Purification Of Extension Products

After the sequencing reaction the extension products are desirably separated from the unincorporated Dye Terminators which would otherwise interfere with the fluorescence-based detection process of the electrophoretically separated sequencing fragments.

For each sequencing reaction, 50 μ g (5 μ l) Streptavidin-coated Dynabeads M-280 (Dynal Inc., Oslo, Norway) may be washed in 5 μ l of 2x Binding and Washing buffer ("B&W"; 2X B&W buffer: 2M NaCl, 10mM Tris-HCl pH 7.5, 1mM EDTA). The beads may then be resuspended in 20 μ l of 2x B&W.

To each 20 μ l sequencing reaction, 20 μ l of resuspended beads may be added, and the mixture may be incubated at room temperature (20-25 C) for 15 minutes. The beads may then be immobilized, the supernatant may be removed, and then the beads may be washed once in 70% ethanol by pipetting up and down five times. Then, as much as possible of the ethanol may desirably be removed, because residual ethanol may interfere with electrophoretic gel mobility.

For each sequencing reaction, 4 μ l of loading buffer (5:1 Formamide-

25mM EDTA pH 8.0, 50mg/ml Dextran Blue) may be added.

8.4. Electrophoresis And Data Collection

Samples prepared by the foregoing methods may be used immediately or be stored at 4 C at least for 24 hours before starting the electrophoretic separation. Prior to the electrophoretic separation, each reaction may be incubated at 90 C for 2 minutes. 3 μ l of each sample may be loaded on a prerun sequencing gel. For an automated ABI 377 sequencer (Applied Biosystems, Foster City, CA) a 0,2mm thick 5% polyacrylamide (acrylamide:bisacrylamide = 29:1) - 7 M urea gel may be used [gel composition: 21.0 g urea, 8.4 ml 30% acrylamide (stock solution: 58g acrylamide, 2g bisacrylamide in bidistilled water), 6.0 ml TBE buffer (10x TBE-buffer: 108.0 g tris base, 55.0 g boric acid, 7.4 g Na2EDTA), 15 μ l TEMED, 350 μ l 10% Ammoniumpersulfate (1.0 g Ammoniumpersulfate in 10 ml ddH₂O), 20.0 ml ddH₂O]. Electrophoresis may be run at constant 48 watt for 8h. Data collection may be initiated immediately after starting the electrophoresis on the ABI377. Data analyses may be performed thereafter using the ABI analysis software (version 2.1.1).

8.5. Data Interpretation And HLA Typing

After data collection, the chromatograms may be printed and sequences may be compared manually to existing HLA data in the EMBL databank and the sequences compiled by Arnett and Parham. Due to the group-specific amplification and the lack of heterozygous positions, manual analysis is typically very fast. Alternatively, sequences may be checked with the data analysis editor (Sequence NavigatorTM, Applied Biosystems) and aligned with any sequence alignment program.

Various publications are cited herein, the contents of which are hereby incorporated by reference in their entireties.

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT:

(ii) TITLE OF THE INVENTION: Method and Kit for HLA Class I Typing

(iii) NUMBER OF SEQUENCES: 245

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Baker & Botts, L.L.P.
- (B) STREET: 30 Rockefeller Plaza
- (C) CITY: New York
- (D) STATE: NY
- (E) COUNTRY: U.S.A.
- (F) ZIP: 10112-0228

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Diskette
- (B) COMPUTER: IBM Compatible
- (C) OPERATING SYSTEM: ASCII DOS text
- (D) SOFTWARE: FastSEQ Version 2.0

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER:
- (B) FILING DATE:
- (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/766,189
- (B) FILING DATE: 12 DEC 1996

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Tenser, Arthur and Kole, Lisa
- (B) REGISTRATION NUMBER: 18,839 and 35,225
- (C) REFERENCE/DOCKET NUMBER: 30861

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 212-705-5000
- (B) TELEFAX: 212-705-5020
- (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (iii) HYPOTHETICAL: no
 (iv) ANTI-SENSE: no
 (v) ORIGINAL SOURCE:
 (A) ORGANISM: human
 (ix) FEATURE:
 (A) NAME/KEY: HLA-A 5' Flanking Region Allele

consensus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAGCCGCAGA CCCCTCTTAG ACTCAGGGCC ACCCACGCAC	GCCTGAAATC TTGGCGCTGG	60
CGCTGCTGTG ACTAACCGAA GAGACCTTTG GGCTGTGGGT	TACCCCTCACT CTTGACCCAG	120
GCGCAGCACT CATAGGTCT TCTTCCTGGG ATGTATCCAA	CCCTCTCCCT CTTTTCTTTG	180
ACGCCTCAAC CCCTTAGGGG TTCCGACCCCT GAGGGGTTAG	GTATGTGGCG GAAGCCCCGG	240
ACTCTGGGAC TCTCGGTGCG GACCCCGGG A	CCCTGAAGCG GGACTGGGGA GACGAGGACA	300
CGGTCGCGA GACAGAGTTA CAGAGGGACT CAGAACCGGG	TTCTCGACAG ACTCTTTGTT	360
CCCTCTTTG GGAGCCGTAC CCGGGGCAGG GAGAGGAAAG	TGAAAAGTAG GGCATTAGAG	420
ACAGGGACTT GACCTGAGGG ACTGAGGGTG		450

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 450 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (iii) HYPOTHETICAL: no
 (iv) ANTI-SENSE: no
 (v) ORIGINAL SOURCE:
 (A) ORGANISM: human
 (ix) FEATURE:
 (A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 0101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GAGCCGCAGA CCCCTCTTAG ACTCAGGGCC ACCCACGCAC	GCCTGAAATC TTGTCGCTGG	60
CGCTGCTGTG ACTAACCGAA GAGACCTTTG GGCTGTGGGT	TACCCCTCACT CTTGACCCAG	120
GCGCAGCACT CATAGGTCT TCTTCCTGGG ATGCATCCAA	CCCTCTCCCT CTTTTCTTTG	180
ACGCCTCAAC CCCTTAGGGG TTCCGACCCCT GAGGGGTTAG	GTATGTGGCG GAAGCCCCGG	240
ACTCTGGGAC TCTCGGTGCG GACCCCGGG A	CCCTGAAGCG GGACTGGGGA GACGAGGACA	300
CGCTTCGCGA GACAGAGTTA CAGAGGGACT CAGAACCGGG	TCCTCGACAG ACTCTTTGTT	360
CCCTCTTTG GGAGCCGTAC CCGGGGCAGG GAGAGGAAAG	TGAAAAGTAG GGTAAATAGAG	420
ACAGGGACTT GACCTGAGGG ACTGAGGGTG		450

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 450 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: genomic DNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 0301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAGCCGCAGA CCCCTCTTAG ACTCAGGGCC ACCCACGCAC GCCCGAAATC TTGTCGCTGG	60
CGCTGCTGTG ACTAACCGAA GAGACCTTG GGCTGTGGGT TACCCCTCACT CTTGACCCAG	120
GCGCAGCACT CATAGGTCT ACTTCCTGGG ATGCATCCAA CCCTCTCCCT CTTTTCTTTG	180
ACGCCTCAAC CCCTTAGGGG TTCCGACCCCT GAGGGGTTAG GTATGTGGCG GAAGCCCCGG	240
ACTCTGAGAC TCTCGGTGCG GACCCCGGG CCCTGAAGCG GGACTGGGGA GACGAGGACA	300
CGCTTCGCGA GACAGAGTTA CAGAGGGACT CAGAACCGGG TCCTCGACAG ACTCTTGTT	360
CCCTCTTTG GGAGCCGTAC CCGGGGCAGG GAGAGGAAAG TGAAAAGTAG GGTAATAGAG	420
ACAGGGACTT GACCTGAGGG ACTGAGGGTG	450

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 450 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 1101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GAGCCCCAGA CCCCTCTTAG ACTCAGGGCC ACCCACGCAC GCCTGAAATC TTCTCGCTGG	60
CGCTTCTGTG ACTAACCGAA GAGACCTTG GGCTGTGGGT TACCCCTCACT CTTGACCCAG	120
GCGCAGCACT CATAGGTCT ACTTCCTGGG ATGCATCCAA CCCTCTCCCT CTTTTCTTTG	180
ACGCCTCAAC CCCTTAGGGG TTCCGACCCCT GAGGGGTTAG GTATGTGGCG GAAGCCCCGG	240
ACTCTGGGAC TCTCGGTGCG GACCCCGGG CCCTGAAGCG GGACTGGGGA GACGAGAACA	300
CGCTTCGCGA GACAGAGTTA CAGAGGGACT CAGAACCGGG TCCTCGACAG ACTCTTGTT	360
CCCTCTTTG GGAGCCGTAC CCGGGGCAGG GAGAGGAAAG TGAAAAGTAG GGTAATAGAG	420
ACAGGGACTT GACCTGAGGG ACTGAGGGTG	450

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 450 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no

- (iv) ANTI-SENSE: no
- (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: HLA-A 5' Flanking Region Allele A*1102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAGCCCCAGA CCCCTTTAG ACTCAGGGCC ACCCACGCAC GCCTGAAATC TTCTCGCTGG	60
CGCTCTGTG ACTAACCGAA GAGACCTTG GGCTGTGGGT TACCCCTCACT CTTGACCCAG	120
GCGCAGCACT CATAGGTCT ACTTCCTGGG ATGCATCCAA CCCTCTCCCT CTTTTCTTTG	180
ACGCCTCAAC CCCTTAGGGG TTCCGACCCCT GAGGGGTTAG GTATGTGGCG GAAGCCCCGG	240
ACTCTGGGAC TCTCGGTGCG GACCCCGGGA CCCTGAAGCG GGACTGGGGA GACGAGAACAA	300
CGCTTCGCGA GACAGAGTTA CAGAGGGACT CAGAACCGGG TTCTCGACAG ACTCTTTGTT	360
CCCTCTTTG GGAGCCGTAC CCGGGGCAGG GAGAGGAAAG TGAAAAGTAG GGTAAATAGAG	420
ACAGGGACTT GACCTGAGGG ACTGAGGGTG	450

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 450 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 3001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GAGCCGCAGA CCCCTTTAG ACTCAGGGCC ACCCACGCAC GCCCGAAATC TTGTCGCTGG	60
CGCTGCTGTG ACTAACCGAA GAGACCTTG GGCTGTGGGT TACCCCTCACT CTTGACCCAG	120
GCGCAGCACT CATAGGTCT ACTTCCTGGG ATGCATCCAA CCCTCTCCCT CTTTTCTTTG	180
ACGCCTCAAC CCCTTAGGGG TTCCGACACT GAGGGGTTAG GTATGTGGCG GAAGCCCCGG	240
ACTCTGGGAC TCTCGGTGCG GACCCCGGGA CCCTGAAGCG GGACTGGGGA GACGAGGACA	300
CGCTTCGCGA GACAGAGTTA CAGAGGGACT CAGAACCGGG TTCTCGACAG ACTCTTTGTT	360
CCCTCTTTG GGAGCCGTAC CCGGGGCAGG GAGAGGAAAG TGAAAAGTAG GGTAAATAGAG	420
ACAGGGACTT GACCTGAGGG ACTGAGGGTG	450

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 450 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human

(ix) FEATURE:

(A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 3002

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAGCCGCAGA CCCCTCTTAG ACTCAGGGCC ACCCACGCAC	60
GGCCGAAATC TTGTCGCTGG	
CGCTGCTGTG ACTAACCGAA GAGACCTTG GGCTGTGGGT TACCCTCACT	120
CTTGACCCAG	
GCGCAGCACT CATAGGTCT ACTTCCTGGG ATGCATCCAA CCCTCTCCCT	180
CTTTTCTTTG	
ACGCCTCAAC CCCTTAGGGG TTCCGACACT GAGGGGTTAG GTATGTGGCG	240
GAAGCCCCGG	
ACTCTGGGAC TCTCGGTGCG GACCCCGGG CCCTGAAGCG GGACTGGGGA	300
GACGAGGACA	
CGCTTCGCGA GACAGAGTTA CAGAGGGACT CAGAACCGGG TTCTCGACAG	360
ACTCTTTGTT	
CCCTCTTTG GGAGCCGTAC CCGGGGCAGG GAGAGGAAAG TGAAAAGTAG GGTAATAGAG	420
ACAGGGACTT GACCTGAGGG ACTGAGGGTG	450

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human

(ix) FEATURE:

(A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 3004

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GAGCCGCAGA CCCCTCTTAG ACTCAGGGCC ACCCACGCAC	60
GGCCGAAATC TTGTCGCTGG	
CGCTGCTGTG ACTAACCGAA GAGACCTTG GGCTGTGGGT TACCCTCACT	120
CTTGACCCAG	
GCGCAGCACT CATAGGTCT ACTTCCTGGG ATGCATCCAA CCCTCTCCCT	180
CTTTTCTTTG	
ACGCCTCAAC CCCTTAGGGG TTCCGACACT GAGGGGTTAG GTATGTGGCG	240
GAAGCCCCGG	
ACTCTGGGAC TCTCGGTGCG GACCCCGGG CCCTGAAGCG GGACTGGGGA	300
GACGAGGACA	
CGCTTCGCGA GACAGAGTTA CAGAGGGACT CAGAACCGGG TTCTCGACAG	360
ACTCTTTGTT	
CCCTCTTTG GGAGCCGTAC CCGGGGCAGG GAGAGGAAAG TGAAAAGTAG GGTAATAGAG	420
ACAGGGACTT GACCTGAGGG ACTGAGGGTG	450

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human

(ix) FEATURE:

(A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 0201-

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GAGCCGCAGA CCCCTCTTAG ACTCAGGGCC ACCCACGCAC GCCTGAAATC TTGGCGCTGG	60
CGCTGCTGTG ACTAACCGAA GAGACCTTG GGCTGTGGGT TACCCCTCACT CTTGACCCAG	120
GCGCAGCACT CATAGGTCT ACTTCCTGGG ATGTATCAA CCCTCTCCCT CTTTCTTTG	180
ACGCCTCAAC CCCTTAGGGG TTCCGACCCCT GAGGGGTTAG GTATGTGGCG GAAGCCCCGG	240
ACTCTGGGAC TCTCGGTGCG GACCCCGGG A CCTGAAGCG GGACTGGGGA GACGAAGACA	300
CGGTTCGCGA GACAGAGTTA CAGAGGGACT CAGAACCGGG TTCTCGACAG ACTCTTTGTT	360
CCCTCTTTGG GAGCCGTACC CGGGGCAGGG AGAGGAAAGT GAAAAATAGG GCATTAGAGA	420
CAGGGACTTG ACCTGAGGGGA CTGAGGGTG	449

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 0215

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GAGCCGCAGA CCCCTCTTAG ACTCAGGGCC ACCCACGCAC GCCTGAAATC TTGGCGCTGG	60
CGCTGCTGTG ACTAACCGAA GAGACCTTG GGCTGTGGGT TACCCCTCACT CTTGACCCAG	120
GCGCAGCACT CATAGGTCT TCTTCCTGGG ATGTATCAA CCCTCTCCCT CTTTCTTTG	180
ACGCCTCAAC CCCTTAGGGG TTCCGACCCCT GAGGGGTTAG GTATGTGGCG GAAGCCCCGG	240
ACTCTGGGAC TCTCGGTGCG GACCCCGGG CCCTGAAGCG GGACTGGGGA GACGAAGACA	300
CGGTTCGCGA GACAGAGTTA CAGAGGGACT CAGAACCGGG TTCTCGACAG ACTCTTTGTT	360
CCCTCTTTGG GAGCCGTACC CGGGGCAGGG AGAGGAAAGT GAAAAATAGG GCATTAGAGA	420
CAGGGACTTG ACCTGAGGGGA CTGAGGGTG	449

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 0217

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GAGCCGCAGA CCCCTCTTAG ACTCAGGGCC ACCCACGCAC GCCTGAAATC TTGGCGCTGG	60
CGCTGCTGTG ACTAACCGAA GAGACCTTG GGCTGTGGGT TACCCCTCACT CTTGACCCAG	120
GCGCAGCACT CATAGGTCT TCTTCCTGGG ATGTATCCAA CCCTCTCCCT CTTTTCTTTG	180
ACGCCTCAAC CCCTTAGGGG TTCCGACCCCT GAGGGGTTAG GTATGTGGCG GAAGCCCCGG	240
ACTCTGGGAC TCTCGGTGCG GACCCCGGG A CCTGAAGCG GGACTGGGGA GACGAAGACA	300
CGGTTCGCGA GACAGAGTTA CAGAGGGACT CAGAACCGGG TTCTCGACAG ACTCTTTGTT	360
CCCTCTTTGG GAGCCGTACC CGGGGCAGGG AGAGGAAAGT GAAAAATAGG GCATTAGAGA	420
CAGGGACTTG ACCTGAGGGGA CTGAGGGTG	449

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 6801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GAGCCGCAGA CCCCTCTTAG ACTCAGGGCC ACCCACGCAC GCCTGAAATC TTGGCGCTGG	60
CGCTGCTGTG ACTAACCGAA GAGACCTTG GGCTGTGGGT TACCCCTCACT CTTGACCCAG	120
GCGCAGCACT CATAGGTCT TCTTCCTGGG ATGTATCCAA CCCTCTCCCT CTTTTCTTTG	180
ACGCCTCAAC CCCTTAGGGG TTCCGACCCCT GAGGGGTTAG GTATGTGGCG GAAGCCCCGG	240
ACTCTGGGAC TCTCGGTGCG GACCCCGGG A CCTGAAGCG GGACTGGGGA GACGAGGACA	300
CGGTTCGCGA GACAGAGTTA CAGAGGGACT CAGAACCGGG TTCTCGACAG ACTCTTTGTA	360
CCCTCTTTGG GAGCCGTACC CGGGGCAGGG AGAGGAAAGT GAAAAATAGG GCATTAGAGA	420
CAGGGACTTG ACCTGAGGGGA CTGAGGGTG	449

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 6802

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAGCCGCAGA CCCCTCTTAG ACTCAGGGCC ACCCACGCAC GCCTGAAATC TTGGCGCTGG	60
CGCTGCTGTG ACTAACCGAA GAGACCTTTG GGCTGTGGGT TACCCTCACT CTTGACCCAG	120
GCGCAGCACT CATAGGTCTT TCTTCCTGGG ATGTATCCAA CCCTCTCCCT CTTTTCTTTG	180
ACGCCTCAAC CCCTTAGGGG TTCCGACCCCT GAGGGTTAG GTATGTGGCG GAAGCCCCGG	240
ACTCTGGGAC TCTCGGTGCG GACCCCGGG CCCTGAAGCG GGACTGGGGA GACGAGGACA	300
CGGTTCGCGA GACAGAGTTA CAGAGGGACT CAGAACCGGG TTCTCGACAG ACTCTTTGTA	360
CCCTCTTGG GAGCCGTACC CGGGGCAGGG AGAGGAAAGT GAAAAATAGG GCATTAGAGA	420
CAGGGACTTG ACCTGAGGGGA CTGAGGGTG	449

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 6901

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GAGCCGCAGA CCCCTCTTAG ACTCAGGGCC ACCCACGCAC GCCTGAAATC TTGGCGCTGG	60
CGCTGCTGTG ACTAACCGAA GAGACCTTTG GGCTGTGGGT TACCCTCACT CTTGACCCAG	120
GCGCAGCACT CATAGGTCTT TCTTCCTGGG ATGTATCCAA CCCTCTCCCT CTTTTCTTTG	180
ACGCCTCAAC CCCTTAGGGG TTCCGACCCCT GAGGGTTAG GTATGTGGCG GAAGCCCCGG	240
ACTCTGGGAC TCTCGGTGCG GACCCCGGG CCCTGAAGCG GGACTGGGGA GACGAGGACA	300
CGGTTCGCGA GACAGAGTTA CAGAGGGACT CAGAACCGGG TTCTCGACAG ACTCTTTGTA	360
CCCTCTTGG GAGCCGTACC CGGGGCAGGG AGAGGAAAGT GAAAAATAGG GCATTAGAGA	420
CAGGGACTTG ACCTGAGGGGA CTGAGGGTG	449

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 2301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GAGCCGCAGA CCCCTCTTAG ACTCAGGGCC ACCCACGCAC GCCTGAAATC TTGTCGCTGG	60
CGCTGCTGTG ACTAACCGAA GAGACCTTTG GGCTGTGGGT TACCCTCACT CTTGACCCAG	120

GGCGCAGCACT CATAGGTCTTGGG ATGTATCCAA CCCTCTCCCT CTTTCTTTG	180
ACGCCTCAAC CCCTTAGGGG TTCCGACCCCT GAGGGGTTAG GTATGTGGCG GAAGCCCCGG	240
ACTCTGGGAC TCTCGGTGCG GACCCCGGGA CCCTGAAGCG GGACTGGGGA GACGAAGACA	300
CGGTTCGCGA GACAGAGTTA CAGAGGGACT TAGAACCGGG TTCTCGACAG ACTCTTTGTT	360
CCCTCTTTG GGAGCCGTAC CCGGGGCAGG GAGAGGAAAG TGAAAAGTAG GGCATTAGAG	420
ACAGGGACTT GACCTGAGGG ACTGAGGGTG	450

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 2402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GAGCCGCAGA CCCCTCTTAG ACTCAGGGCC ACCCACGCAC GCCTGAAATC TTGTCGCTGG	60
CGCTGCTGTG ACTAACCGAA GAGACCTTTG GGCTGTGGGT TACCCCTCACT CTTGACCCAG	120
GCGCAGCACT CATAGGTCTTGGG ATGTATCCAA CCCTCTCCCT CTTTCTTTG	180
ACGCCTCAAC CCCTTAGGGG TTCCGACCCCT GAGGGGTTAG GTATGTGGCG GAAGCCCCGG	240
ACTCTGGGAC TCTCGGTGCG GACCCCGGGA CCCTGAAGCG GGACTGGGGA GACGAAGACA	300
CGGTTCGCGA GACAGAGTTA CAGAGGGACT TAGAACCGGG TTCTCGACAG ACTCTTTGTT	360
CCCTCTTTG GGAGCCGTAC CCGGGGCAGG GAGAGGAAAG TGAAAAGTAG GGCATTAGAG	420
ACAGGGACTT GACCTGAGGG ACTGAGGGTG	450

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 2403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GAGCCGCAGA CCCCTCTTAG ACTCAGGGCC ACCCACGCAC GCCTGAAATC TTGTCGCTGG	60
CGCTGCTGTG ACTAACCGAA GAGACCTTTG GGCTGTGGGT TACCCCTCACT CTTGACCCAG	120
GCGCAGCACT CATAGGTCTTGGG ATGTATCCAA CCCTCTCCCT CTTTCTTTG	180
ACGCCTCAAC CCCTTAGGGG TTCCGACCCCT GAGGGGTTAG GTATGTGGCG GAAGCCCCGG	240

ACTCTGGGAC TCTCGGTGCG GACCCGGGA CCCTGAAGCG GGACTGGGGA GACGAAGACA	300
CGGTTCGCGA GACAGAGTTA CAGAGGGACT TAGAACCGGG TTCTCGACAG ACTCTTGTT	360
CCCTCTTTG GGAGCCGTAC CCGGGGCAGG GAGAGGAAAG TGAAAAGTAG GGCATTAGAG	420
ACAGGGACTT GACCTGAGGG ACTGAGGGTG	450

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(v) ORIGINAL SOURCE:

(A) ORGANISM: human

(ix) FEATURE:

(A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 2404

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GAGCCGCAGA CCCCTCTTAG ACTCAGGGCC ACCCACGCAC GCCTGAAATC TTGTCGCTGG	60
CGCTGCTGTG ACTAACCGAA GAGACCTTG GGCTGTGGGT TACCTCACT CTTGACCCAG	120
GCGCAGCACT CATAGGTCTT TCTTCCTGGG ATGTATCCAA CCCTCTCCCT CTTTCTTTG	180
ACGCCTCAAC CCCTTAGGGG TTCCGACCT GAGGGGTTAG GTATGTGGCG GAAGCCCCGG	240
ACTCTGGGAC TCTCGGTGCG GACCCGGGA CCCTGAAGCG GGACTGGGGA GACGAAGACA	300
CGGTTCGCGA GACAGAGTTA CAGAGGGACT TAGAACCGGG TTCTCGACAG ACTCTTGTT	360
CCCTCTTTG GGAGCCGTAC CCGGGGCAGG GAGAGGAAAG TGAAAAGTAG GGCATTAGAG	420
ACAGGGACTT GACCTGAGGG ACTGAGGGTG	450

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(v) ORIGINAL SOURCE:

(A) ORGANISM: human

(ix) FEATURE:

(A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 2405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GAGCCGCAGA CCCCTCTTAG ACTCAGGGCC ACCCACGCAC GCCTGAAATC TTGTCGCTGG	60
CGCTGCTGTG ACTAACCGAA GAGACCTTG GGCTGTGGGT TACCTCACT CTTGACCCAG	120
GCGCAGCACT CATAGGTCTT TCTTCCTGGG ATGTATCCAA CCCTCTCCCT CTTTCTTTG	180
ACGCCTCAAC CCCTTAGGGG TTCCGACCT GAGGGGTTAG GTATGTGGCG GAAGCCCCGG	240
ACTCTGGGAC TCTCGGTGCG GACCCGGGA CCCTGAAGCG GGACTGGGGA GACGAAGACA	300
CGGTTCGCGA GACAGAGTTA CAGAGGGACT TAGAACCGGG TTCTCGACAG ACTCTTGTT	360

CCCTCTTTG GGAGCCGTAC CCGGGGCAGG GAGAGGAAAG TGAAAAGTAG GGCATTAGAG	420
ACAGGGACTT GACCTGAGGG ACTGAGGGTG	450

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 2407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GAGCCGCAGA CCCCTCTTAG ACTCAGGGCC ACCCACGCAC GCCTGAAATC TTGTCGCTGG	60
CGCTGCTGTG ACTAACCGAA GAGACCTTTG GGCTGTGGGT TACCCCTCACT CTTGACCCAG	120
GCGCAGCACT CATAGGTCTT TCTTCCTGGG ATGTATCCAA CCCTCTCCCT CTTTTCTTTG	180
ACGCCTCAAC CCCTTAGGGG TTCCGACCCCT GAGGGGTTAG GTATGTGGCG GAAGCCCCGG	240
ACTCTGGGAC TCTCGGTGCG GACCCCGGG A CCCTGAAGCG GGACTGGGGA GACGAAGACA	300
CGGTTCGCGA GACAGAGTTA CAGAGGGACT TAGAACCGGG TTCTCGACAG ACTCTTTGTT	360
CCCTCTTTG GGAGCCGTAC CGGGGGCAGG GAGAGGAAAG TGAAAAGTAG GGCATTAGAG	420
ACAGGGACTT GACCTGAGGG ACTGAGGGTG	450

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 2501

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GAGCCGCAGA CCCCTCTTAG ACTCAGGGCC ACCCACGCAC GCCTGAAATC TTGGCGCTGG	60
CGCTGCTGTG ACTAACCGAA GAGACCTTTG GGCTGTGGGT TACCCCTCACT CTTGACCCAG	120
GCGCAGCACT CATAGGTCTT TCTTCCTGGG ATGTATCCAA CCCTCTCCCT CTTTTCTTTG	180
ACGCCTCAAC CCCTTAGGGG TTCCGACCCCT GAGGGGTTAG GTATGTGGCG GAAGCCCCGG	240
ACTCTGGGAC TCTCGGTGCG GACCCCGGG A CCCTGAAGCG GGACTGGGGA GACGAGGACA	300
CGGTTCGAGA GACAGAGTTA CAGAGGGACT CAGAACCGGG TTCTCGACAG ACTCTTTGTT	360
CCCTCTTTG GGAGCCGTAC CGGGGGCAGG GAGAGGAAAG TGAAAAGTAG GGCATTAGAG	420
ACAGGGACTT GACCTGAGGG ACTGAGGGTG	445

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 2601

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GAGCCGCAGA CCCCTCTTAG ACTCAGGGCC ACCCACGCAC GCCTGAAATC TTGGCGCTGG	60
CGCTGCTGTG ACTAACCGAA GAGACCTTG GGCTGTGGGT TACCCCTCACT CTTGACCCAG	120
GCGCAGCACT CATAGGTCT TCTTCCTGGG ATGTATCCAA CCCTCTCCCT CTTTTCTTTG	180
ACGCCTCAAC CCCTTAGGGG TTCCGACCT GAGGGGTTAG GTATATGGCG GAAGCCCCGG	240
ACTCTGGGAC TCTCGGTGCG GACCCCGGG CCCTGAAGCG GGACTGGGGA GACGAGGACA	300
CGGTTCGCGA GACAGAGTTA CAGAGGGACT CAGAACCGGG TTCTCGACAG ACTCTTTGTT	360
CCCTCTTTG GGAGCGTAC CGGGGGCAGG GAGAGGAAAG TGAAAAATAG GGCATTAGAG	420
ACAGGGACTT GACCTGAGGG ACTGAGGGTG	450

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 3402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GAGCCGCAGA CCCCTCTTAG ACTCAGGGCC ACCCACGCAC GCCTGAAATC TTGGCGCTGG	60
CGCTGCTGTG ACTAACCGAA GAGACCTTG GGCTGTGGGT TACCCCTCACT CTTGACCCAG	120
GCGCAGCACT CATAGGTCT TCTTCCTGGG ATGTATCCAA CCCTCTCCCT CTTTTCTTTG	180
ACGCCTCAAC CCCTTAGGGG TTCCGACCT GAGGGGTTAG GTATGTGGCG GAAGCCCCGG	240
ACTCTGGGAC TCTCGGTGCG GACCCCGGG CCCTGAAGCG GGACTGGGGA GACGAGGACA	300
CGGTTCGCGA GACAGAGTTA CAGAGGGACT CAGAACCGGG TTCTCGACAG ACTCTTTGTT	360
CCCTCTTTG GAGCCGTAC CGGGGGCAGG AGAGGAAAGT GAAAAATAGG GCATTAGAGA	420
CAGGGACTTG ACCTGAGGG A CTGAGGGTG	449

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 4301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GAGCCGCAGA CCCCTCTTAG ACTCAGGGCC ACCCACGCAC GCCTGAAATC TTGGCGCTGG	60
CGCTGCTGTG ACTAACCGAA GAGACCTTTG GGCTGTGGGT TACCCCTCACT CTTGACCCAG	120
GCGCAGCACT CATAGGTCTT CTTCTCTGGG ATGTATCCAA CCCTCTCCCT CTTTTCTTTG	180
ACGCCTCAAC CCCTTAGGGG TTCCGACCCCT GAGGGGTTAG GTATATGGCG GAAGCCCCGG	240
ACTCTGGGAC TCTCGGTGCG GACCCCGGG CCCTGAAGCG GGACTGGGGA GACGAGGACA	300
CGGTTCGCGA GACAGAGTTA CAGAGGGACT CAGAACCGGG TTCTCGACAG ACTCTTTGTT	360
CCCTCTTTGG GAGCCGTACC CGGGGCAGGG AGAGGAAAGT GAAAAATAGG GCATTAGAGA	420
CAGGGACTTG ACCTGAGGGGA CTGAGGGTG	449

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 6601

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GAGCCGCAGA CCCCTCTTAG ACTCAGGGCC ACCCACGCAC GCCTGAAATC TTGGCGCTGG	60
CGCTGCTGTG ACTAACCGAA GAGACCTTTG GGCTGTGGGT TACCCCTCACT CTTGACCCAG	120
GCGCAGCACT CATAGGTCTT CTTCTCTGGG ATGTATCCAA CCCTCTCCCT CTTTTCTTTG	180
ACGCCTCAAC CCCTTAGGGG TTCCGACCCCT GAGGGGTTAG GTATATGGCG GAAGCCCCGG	240
ACTCTGGGAC TCTCGGTGCG GACCCCGGG CCCTGAAGCG GGACTGGGGA GACGAGGACA	300
CGGTTCGCGA GACAGAGTTA CAGAGGGACT CAGAACCGGG TTCTCGACAG ACTCTTTGTT	360
CCCTCTTTGG GAGCCGTACC CGGGGCAGGG AGAGGAAAGT GAAAAATAGG GCATTAGAGA	420
CAGGGACTTG ACCTGAGGGGA CTGAGGGTG	449

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 6602

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GAGCCGCAGA CCCCTCTTAG ACTCAGGGCC ACCCACGCAC GCCTGAAATC TTGGCGCTGG	60
CGCTGCTGTG ACTAACCGAA GAGACCTTG GGCTGTGGGT TACCCCTCACT CTTGACCCAG	120
GCGCAGCACT CATAGGTCT TCTTCCTGGG ATGTATCAA CCCTCTCCCT CTTTTCTTTG	180
ACGCCTCAAC CCCTTAGGGG TTCCGACCCCT GAGGGGTTAG GTATGTGGCG GAAGCCCCGG	240
ACTCTGGGAC TCTCGGTGCG GACCCCGGGA CCCTGAAGCG GGACTGGGGA GACGAGGACA	300
CGGTCGCGA GACAGAGTTA CAGAGGGACT CAGAACCGGG TTCTCGACAG ACTCTTTGTA	360
CCCTCTTGG GAGCCGTACC CGGGGCAGGG AGAGGAAAGT GAAAAATAGG GCATTAGAGA	420
CAGGGACTTG ACCTGAGGGGA CTGAGGGTG	449

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 449 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 6603

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GAGCCGCAGA CCCCTCTTAG ACTCAGGGCC ACCCACGCAC GCCTGAAATC TTGGCGCTGG	60
CGCTGCTGTG ACTAACCGAA GAGACCTTG GGCTGTGGGT TACCCCTCACT CTTGACCCAG	120
GCGCAGCACT CATAGGTCT TCTTCCTGGG ATGTATCAA CCCTCTCCCT CTTTTCTTTG	180
ACGCCTCAAC CCCTTAGGGG TTCCGACCCCT GAGGGGTTAG GTATGTGGCG GAAGCCCCGG	240
ACTCTGGGAC TCTCGGTGCG GACCCCGGGA CCCTGAAGCG GGACTGGGGA GACGAGGACA	300
CGGTCGCGA GACAGAGTTA CAGAGGGACT CAGAACCGGG TTCTCGACAG ACTCTTTGTA	360
CCCTCTTGG GAGCCGTACC CGGGGCAGGG AGAGGAAAGT GAAAAATAGG GCATTAGAGA	420
CAGGGACTTG ACCTGAGGGGA CTGAGGGTG	449

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 450 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (iii) HYPOTHETICAL: no
 (iv) ANTI-SENSE: no
 (v) ORIGINAL SOURCE:
 (A) ORGANISM: human
 (ix) FEATURE:
 (A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 2901

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GAGCCGCAGA CCCCTCTTAG ACTCAGGGCC ACCCACGCAC GCCTGAAATC TTGGCGCTGG	60
CGCTGCTGTG ACTAACCGAA GAGACCTTTG GGCTGTGGGT TACCCCTCACT CTTGACCCAG	120
GCGCAGCACT CATAGGTCTT TCTTCCTGGG ATGTATCCAA CCGTCTCCCT CTTTTCTTTG	180
ACGCCTCAAC CCCTTAGGGG TTCCGACCCCT GAGGGGTTAG GTATGTGGCG GAAGCCCCGG	240
ACTCTGGGAC TCTCGGTGCG GACCCCGGA CCCTGAAGCG GGACTGGGGA GACGAGGACA	300
CGGTTCGAGA GACAGAGTTA CAGAGGGACT CAGAACCCGGG TTCTCGACAG ACTCTTTGTT	360
CCCTCTTTG GGAGCCGTAC CCGGGGCAGG GAGAGGAAAG TGAAAAGTAG GGCATTAGAG	420
ACAGGGACTT GACCTGAGGG ACTGAGGGTG	450

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 450 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (iii) HYPOTHETICAL: no
 (iv) ANTI-SENSE: no
 (v) ORIGINAL SOURCE:
 (A) ORGANISM: human
 (ix) FEATURE:
 (A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 2902

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GAGCCGCAGA CCCCTCTTAG ACTCAGGGCC ACCCACGCAC GCCTGAAATC TTGGCGCTGG	60
CGCTGCTGTG ACTAACCGAA GAGACCTTTG GGCTGTGGGT TACCCCTCACT CTTGACCCAG	120
GCGCAGCACT CATAGGTCTT TCTTCCTGGG ATGTATCCAA CCGTCTCCCT CTTTTCTTTG	180
ACGCCTCAAC CCCTTAGGGG TTCCGACCCCT GAGGGGTTAG GTATGTGGCG GAAGCCCCGG	240
ACTCTGGGAC TCTCGGTGCG GACCCCGGA CCCTGAAGCG GGACTGGGGA GACGAGGACA	300
CGGTTCGAGA GACAGAGTTA CAGAGGGACT CAGAACCCGGG TTCTCGACAG ACTCTTTGTT	360
CCCTCTTTG GGAGCCGTAC CCGGGGCAGG GAGAGGAAAG TGAAAAGTAG GGCATTAGAG	420
ACAGGGACTT GACCTGAGGG ACTGAGGGTG	450

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 450 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: no
 (iv) ANTI-SENSE: no
 (v) ORIGINAL SOURCE:
 (A) ORGANISM: human
 (ix) FEATURE:
 (A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 31012

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GAGCCGCAGA CCCCTCTTAG ACTCAGGGCC ACCCACGCAC GCCTGAAATC TTGGCGCTGG	60
CGCTGCTGTG ACTAACCGAA GAGACCTTG GGCTGTGGGT TACCCCTCACT CTTGACCCAG	120
GCGCAGCACT CATAGGTCT TCTTCCTGGG ATGTATCCAA CCCTCTCCCT CTTTCTTTG	180
ACGCCTCAAC CCCTTAGGGG TTCCGACCCCT GAGGGGTTAG GTATGTGGCG GAAGCCCCGG	240
ACTCTGGGAC TCTCGGTGCG GACCCCGGG A CATGAAGCG GGACTGGGGA GACGAGGACA	300
CGGTTCGCGA GACAGAGTTA CAGAGGGACT CAGAACCGGG TTCTCGACAG ACTCTTGTT	360
CCCTCTTTG GGACCGTAC CCGGGGCAGG GAGAGGAAAG TGAAAAGTAG GGCATTAGAG	420
ACAGGGACTT GACCTGAGGG ACTGAGGGTG	450

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 449 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (iii) HYPOTHETICAL: no
 (iv) ANTI-SENSE: no
 (v) ORIGINAL SOURCE:
 (A) ORGANISM: human
 (ix) FEATURE:
 (A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 3201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GAGCCGCAGA CCCCTCTTAG ACTCAGGGCC ACCCACGCAC GCCTGAAATC TTGGCGCTGG	60
CGCTGCTGTG ACTAACCGAA GAGACCTTG GGCTGTGGGT TACCCCTCACT CTTGACCCAG	120
GCGCAGCACT CATAGGTCT TCTTCCTGGG ATGTATCCAA CCCTCTCCCT CTTTCTTTG	180
ACGCCTCAAC CCCTTAGGGG TTCCGACCCCT GAGGGGTTAG GTATGTGGCG GAAGCCCCGG	240
ACTCTGGGAC TCTCGGTGCG GACCCCGGG A CCCTGAAGCG GGACTGGGGA GACGAGGACA	300
CGGTTCGCGA GACAGAGTTA CAGAGGGACT CAGAACCGGG TTCTCGACAG ACTCTTGTT	360
CCCTCTTTG GAGCCGTACC CCGGGCAGG AGAGGAAAGT GAAAAGTAGG GCATTAGAGA	420
CAGGGACTTG ACCTGAGGG A CTGAGGGTG	449

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 450 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (iii) HYPOTHETICAL: no
 (iv) ANTI-SENSE: no

(v) ORIGINAL SOURCE:
 (A) ORGANISM: human

(ix) FEATURE:
 (A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 3301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GAGCCGCAGA CCCCTTTAG ACTCAGGGCC ACCCACGCAC	GCCTGAAATC TTGGCGCTGG	60
CGCTGCTGTG ACTAACCGAA GAGACCTTTG GGCTGTGGGT	TACCCCTCACT CTTGACCCAG	120
GCGCAGCACT CATAGGTCT TCTTCCTGGG ATGTATCCAA	CCCTCTCCCT CTTTTCTTTG	180
ACGCCTCAAC CCCTTAGGGG TTCCGACCCCT GAGGGGTTAG	GTATGTGGCG GAAGCCCCGG	240
ACTCTGGGAC TCTCGGTGCG GACCCCGGGA CCATGAAGCG	GGACTGGGGA GACGAGGACA	300
CGGTTCGCGA GACAGAGTTA CAGAGGGACT CAGAACCGGG	TTCTCGACAG ACTCTTGTT	360
CCCTCTTTG GGACCCGTAC CCGGGGCAGG GAGAGGAAAG	TGAAAAGTAG GGCATTAGAG	420
ACAGGGACTT GACCTGAGGG ACTGAGGGTG		450

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 450 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (iii) HYPOTHETICAL: no
 (iv) ANTI-SENSE: no
 (v) ORIGINAL SOURCE:
 (A) ORGANISM: human
 (ix) FEATURE:
 (A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 3303

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GAGCCGCAGA CCCCTTTAG ACTCAGGGCC ACCCACGCAC	GCCTGAAATC TTGGCGCTGG	60
CGCTGCTGTG ACTAACCGAA GAGACCTTTG GGCTGTGGGT	TACCCCTCACT CTTGACCCAG	120
GCGCAGCACT CATAGGTCT TCTTCCTGGG ATGTATCCAA	CCCTCTCCCT CTTTTCTTTG	180
ACGCCTCAAC CCCTTAGGGG TTCCGACCCCT GAGGGGTTAG	GTATGTGGCG GAAGCCCCGG	240
ACTCTGGGAC TCTCGGTGCG GACCCCGGGA CCATGAAGCG	GGACTGGGGA GACGAGGACA	300
CGGTTCGCGA GACAGAGTTA CAGAGGGACT CAGAACCGGG	TTCTCGACAG ACTCTTGTT	360
CCCTCTTTG GGACCCGTAC CCGGGGCAGG GAGAGGAAAG	TGAAAAGTAG GGCATTAGAG	420
ACAGGGACTT GACCTGAGGG ACTGAGGGTG		450

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 449 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (iii) HYPOTHETICAL: no
 (iv) ANTI-SENSE: no
 (v) ORIGINAL SOURCE:
 (A) ORGANISM: human

(ix) FEATURE:

(A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 7401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GAGCCGCAGA CCCCTCTTAG ACTCAGGGCC ACCCACGCAC GCCTGAAATC TTGGCGCTGG	60
CGCTGCTGTG ACTAACCGAA GAGACCTTTG GGCTGTGGGT TACCCCTCACT CTTGACCCAG	120
GCGCAGCACT CATAGGTCT TCTTCCTGGG ATGTATCCAA CCGTCTCCCT CTTTTCTTTG	180
ACGCCTCAAC CCCTTAGGGG TTCCGACCCCT GAGGGGTAG GTATGTGGCG GAAGCCCCGG	240
ACTCTGGGAC TCTCGGTGCG GACCCCGGG A CCTGAAGCG GGACTGGGGA GACGAGGACA	300
CGGTTCCGGA GACAGAGTTA CAGAGGGACT CAGAACCGGG TTCTCGACAG ACTCTTTGTT	360
CCCTCTTTGG GAGCCGTACC CGGGGCAGGG AGAGGAAAGT GAAAAGTAGG GCATTAGAGA	420
CAGGGACTTG ACCTGAGGGGA CTGAGGGTG	449

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: genomic DNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: IL-210m

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

ACCCGGGAAG CGGGGCCT

18

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: genomic DNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 7402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GAGCCGCAGA CCCCTCTTAG ACTCAGGGCC ACCCACGCAC GCCTGAAATC TTGGCGCTGG	60
CGCTGCTGTG ACTAACCGAA GAGACCTTTG GGCTGTGGGT TACCCCTCACT CTTGACCCAG	120
GCGCAGCACT CATAGGTCT TCTTCCTGGG ATGTATCCAA CCGTCTCCCT CTTTTCTTTG	180

ACGCCTCAAC CCCTTAGGGG TTCCGACCCCT GAGGGGTTAG GTATGTGGCG GAAGCCCCGG	240
ACTCTGGGAC TCTCGGTGCG GACCCCGGGA CCCTGAAGCG GGACTGGGGA GACGAGGACA	300
CGGTTCGCGA GACAGAGTTA CAGAGGGACT CAGAACCGGG TTCTCGACAG ACTCTTGTT	360
CCCTCTTGG GAGCCGTACC CGGGGCAGGG AGAGGAAAGT GAAAAGTAGG GCATTAGAGA	420
CAGGGACTTG ACCTGAGGGGA CTGAGGGTG	449

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 7403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GAGCCGCAGA CCCCTCTTAG ACTCAGGGCC ACCCACCGCAC GCCTGAAATC TTGGCGCTGG	60
CGCTGCTGTG ACTAACCGAA GAGACCTTTG GGCTGTGGGT TACCTCTCACT CTTGACCCAG	120
GCGCAGCACT CATAGGTCTT CTTCTCTGGG ATGTATCCAA CCCTCTCCCT CTTTTCTTTG	180
ACGCCTCAAC CCCTTAGGGG TTCCGACCCCT GAGGGGTTAG GTATGTGGCG GAAGCCCCGG	240
ACTCTGGGAC TCTCGGTGCG GACCCCGGGA CCCTGAAGCG GGACTGGGGA GACGAGGACA	300
CGGTTCGCGA GACAGAGTTA CAGAGGGACT CAGAACCGGG TTCTCGACAG ACTCTTGTT	360
CCCTCTTGG GAGCCGTACC CGGGGCAGGG AGAGGAAAGT GAAAAGTAGG GCATTAGAGA	420
CAGGGACTTG ACCTGAGGGGA CTGAGGGTG	449

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 8001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GAGCCGCAGA CCCCTCTTAG ACTCAGGGCC ACCCACCGCAC GCCTGAAATC TTGGCGCTGG	60
CGCTGCTGTG ACTAACCGAA GAGACCTTTG GGCTGTGGGT TACCTCTCACT CTTGACCCAG	120
GCGCAGCACT CATAGGTCTT CTTCTCTGGG ATGTATCCAA CCCTCTCCCT CTTTTCTTTG	180
ACGCCTCAAC CCCTTAGAGG TTCCGACCCCT GAGGGGTTAG GTATGTGGCG GAAGCCCCGG	240
ACTCTGGGAC TCTCGGTGCG GACCCCGGGA CCCTGAAGCG GGACTGGGGA GACGAGGACA	300

CGCTTCGCGA GACAGAGTTA CAGAGGGACT CAGAACCGGG TCCTCGACAG ACTCTTGTT	360
CCCTCTTGG GAGCCGTACC CGGGGCAGGG AGAGGAAAGT GAAAAGTAGG GCATTAGAGA	420
CAGGGACTTG ACCTGAGGGGA CTGAGGGTG	449

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele consensus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GTGAGTGCAG GGTGGGGAGG GAAACGGCCT CTGTGGGAG AAGCAAGGGG CCCGCCTGGC	60
GGGGCGCAG GACCCGGGAA GCCCGGCCGG GAGGAGGGTC GGGCAGGTCT CAGCCACTCC	120
TCGCCCCCAG	130

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A 5' Intron Allele A* 0101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GTGAGTGCAG GGTGGGGAGG GAAACGGCCT CTGCAGGGAG AAGCAAGGGG CCCTCCTGGC	60
GGGGCGCAG GACCCGGGAA GCCCGGCCGG GAGGAGGGTC GGGCAGGTCT CAGCCACTGC	120
TCGCCCCCAG	130

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA

- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 0301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GTGAGTGCAG GGTGGGGAGG GAAACCGCCT CTGCGGGAG AAGCAAGGGG CCCTCCTGGC	60
GGGGCGCAG GACCGGGGA GCCGCGCCGG GACGAGGGTC GGGCAGGTCT CAGCCACTGC	120
TCGCCCCCAG	130

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 130 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 1101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GTGAGTGCAG GGTGGGGAGG GAAACCGCCT CTGCGGGAG AAGCAAGGGG CCCTCCTGGC	60
GGGGCGCAG GACCGGGGA GCCGCGCCGG GAGGAGGGTC GGGCAGGTCT CAGCCACTGC	120
TCGCCCCCAG	130

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 130 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 1102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GTGAGTGCAG GGTGGGGAGG GAAACCGCCT CTGCGGGAG AAGCAAGGGG CCCTCCTGGC	60
GGGGCGCAG GACCGGGGA GCCGCGCCGG GAGGAGGGTC GGGCAGGTCT CAGCCACTGC	120

TCGCCCCCAG

130

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 3001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GTGAGTGCAG GGTGGGGAGG GAAACCGCCT CTGCGGGGAG AAGCAAGGGG CCCTCCTGGC GGGGGCGCAG GACCGGGGGA GCCGCGCCGG GAGGAGGGTC GGTCAAGGTCT CAGCCACTGC TCGCCCCCAG	60 120 130
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(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 3002

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GTGAGTGCAG GGTGGGGAGG GAAACCGCCT CTGCGGGGAG AAGCAAGGGG CCCTCCTGGC GGGGGCGCAG GACCGGGGGA GCCGCGCCGG GAGGAGGGTC GGTCAAGGTCT CAGCCACTGC TCGCCCCCAG	60 120 130
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(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no

(v) ORIGINAL SOURCE:
 (A) ORGANISM: human

(ix) FEATURE:
 (A) NAME/KEY: HLA-A Intron 1 Allele A* 3004

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GTGAGTGCAG GGTGGGAGG GAAACGCCT CTGCGGGAG AAGCAAGGG CCCTCTGGC	60
GGGGCGCAG GACCGGGGA GCCGCGCCGG GAGGAGGGTC GGTCAGGTCT CAGCCACTGC	120
TCGCCCCCAG	130

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 129 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (iii) HYPOTHETICAL: no
 (iv) ANTI-SENSE: no
 (v) ORIGINAL SOURCE:
 (A) ORGANISM: human
 (ix) FEATURE:
 (A) NAME/KEY: HLA-A Intron 1 Allele A* 0201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GTGAGTGCAG GGTGGGAGG GAAACGCCT CTGCGGGAG AAGCAACGGG CCGCCTGGCG	60
GGGGCGCAGG ACCCGGGAAAG CCGCGCCGGG AGGAGGGTCG GGCGGGTCTC AGCCACTCCT	120
CGTCCCCAG	129

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 129 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (iii) HYPOTHETICAL: no
 (iv) ANTI-SENSE: no
 (v) ORIGINAL SOURCE:
 (A) ORGANISM: human
 (ix) FEATURE:
 (A) NAME/KEY: HLA-A Intron 1 Allele A* 0202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GTGAGTGCAG GGTGGGAGG GAAACGCCT CTGCGGGAG AAGCAACGGG CCGCCTGGCG	60
GGGGCGCAGG ACCCGGGAAAG CCGCGCCGGG AGGAGGGTCG GGCGGGTCTC AGCCACTCCT	120
CGTCCCCAG	129

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 129 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(v) ORIGINAL SOURCE:

(A) ORGANISM: human

(ix) FEATURE:

(A) NAME/KEY: HLA-A Intron 1 Allele A* 0203

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GTGAGTGCAG	GGTCGGGAGG	GAAACGGCCT	CTGTGGGGAG	AAGCAACGGG	CCGCCTGGCG	60
GGGGCGCAGG	ACCCGGGAAG	CCGCGCCGGG	AGGAGGGTCG	GGCGGGTCTC	AGCCACTCCT	120
CGTCCCCAG						129

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 129 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(v) ORIGINAL SOURCE:

(A) ORGANISM: human

(ix) FEATURE:

(A) NAME/KEY: HLA-A Intron 1 Allele A* 0204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GTGAGTGCAG	GGTCGGGAGG	GAAACGGCCT	CTGTGGGGAG	AAGCAACGGG	CCGCCTGGCG	60
GGGGCGCAGG	ACCCGGGAAG	CCGCGCCGGG	AGGAGGGTCG	GGCGGGTCTC	AGCCACTCCT	120
CGTCCCCAG						129

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 129 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(v) ORIGINAL SOURCE:

(A) ORGANISM: human

(ix) FEATURE:

(A) NAME/KEY: HLA-A Intron 1 Allele A* 0205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GTGAGTGCAG	GGTCGGGAGG	GAAACGGCCT	CTGTGGGGAG	AAGCAACGGG	CCGCCTGGCG	60
GGGGCGCAGG	ACCCGGGAAG	CCGCGCCGGG	AGGAGGGTCG	GGCGGGTCTC	AGCCACTCCT	120
CGTCCCCAG						129

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 0206

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GTGAGTGCAG	GGTCGGGAGG	GAAACGGCCT	CTGTGGGGAG	AAGCAACGGG	CCGCCTGGCG	60
GGGGCGCAGG	ACCCGGGAAG	CCGCGCCGGG	AGGAGGGTCG	GGCGGGTCTC	AGCCACTCCT	120
CGTCCCCAG						129

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 0207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GTGAGTGCAG	GGTCGGGAGG	GAAACGGCCT	CTGTGGGGAG	AAGCAACGGG	CCGCCTGGCG	60
GGGGCGCAGG	ACCCGGGAAG	CCGCGCCGGG	AGGAGGGTCG	GGCGGGTCTC	AGCCACTCCT	120
CGTCCCCAG						129

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 0207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GTGAGTGCAG GGTGGGAGG GAAACGGCCT CTGTGGGAG AAGCAACGGG CCGCCTGGCG	60
GGGGCGCAGG ACCCGGGAG CCGCGCCGGG AGGAGGGTCG GGCAGGTCTC AGCCACTCCT	120
CGTCCCCAG	129

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 0208

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GTGAGTGCAG GGTGGGAGG GAAACGGCCT CTGTGGGAG AAGCAACGGG CCGCCTGGCG	60
GGGGCGCAGG ACCCGGGAG CCGCGCCGGG AGGAGGGTCG GGCAGGTCTC AGCCACTCCT	120
CGTCCCCAG	129

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 0209

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GTGAGTGCAG	GGTCGGGAGG	GAAACGGCCT	CTGTGGGAG	AAGCAACGGG	CCGCCTGGCG	60
GGGGCGCAGG	ACCCGGGAAG	CCGCGCCGGG	AGGAGGGTCG	GGCGGGTCTC	AGCCACTCCT	120
CGTCCCCAG						129

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 0210

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

GTGAGTGCAG	GGTCGGGAGG	GAAACGGCCT	CTGTGGGAG	AAGCAACGGG	CCGCCTGGCG	60
GGGGCGCAGG	ACCCGGGAAG	CCGCGCCGGG	AGGAGGGTCG	GGCGGGTCTC	AGCCACTCCT	120
CGTCCCCAG						129

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 0211

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GTGAGTGCAG	GGTCGGGAGG	GAAACGGCCT	CTGTGGGAG	AAGCAACGGG	CCGCCTGGCG	60
GGGGCGCAGG	ACCCGGGAAG	CCGCGCCGGG	AGGAGGGTCG	GGCGGGTCTC	AGCCACTCCT	120
CGTCCCCAG						129

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 0215

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GTGAGTGCAG GGTGGGGAGG GAAACGGCCT CTGTGGGGAG AAGCAACGGG CCGCCTGGCG	60
GGGGCGCAGG ACCCGGGAAAG CCGCGCCGGG AGGAGGGTCG GGCGGGTCTC AGCCACTCCT	120
CGTCCCCAG	129

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 129 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 0217

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GTGAGTGCAG GGTGGGGAGG GAAACGGCCT CTGTGGGGAG AAGCAACGGG CCGCCTGGCG	60
GGGGCGCAGG ACCCGGGAAAG CCGCGCCGGG AGGAGGGTCG GGCGGGTCTC AGCCACTCCT	120
CGTCCCCAG	129

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 130 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 6801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GTGAGTGCAG GGTGGGGAGG GAAACGGCCT CTGTGGGGAG AAGCAAGGGG CCCGCCGGC	60
GGGGGCGCAG GACCCGGGAA GCCGCGCCTG GAGGAGGGTC GGGCGGGTCT CAGCCACTCC	120
TCGCCCCCAG	130

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 6802

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

GTGAGTGCAG GGTGGGGAGG GAAACGGCCT CTGTGGGGAG AAGCAAGGGG CCCGCCGGC	60
GGGGGCGCAG GACCCGGGAA GCCGCGCCTG GAGGAGGGTC GGGCGGGTCT CAGCCACTCC	120
TCGCCCCCAG	130

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 6901

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

GTGAGTGCAG GGTGGGGAGG GAAACGGCCT CTGTGGGGAG AAGCAAGGGG CCCGCCGGC	60
GGGGGCGCAG GACCCGGGAA GCCGCGCCTG GAGGAGGGTC GGGCGGGTCT CAGCCACTCC	120
TCGCCCCCAG	130

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA

- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 2301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GTGAGTGCAG GGTGGGAGG GAAACGGCCT CTGCGGGAG AAGCAAGGGG CCCGCCTGGC	60
GGGGCGCAA GACCCGGAA GCCGCGCCGG GAGGAGGGTC GGGCGGGTCT CAGCCACTCC	120
TCGTCCCCAG	130

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 130 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 2402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

GTGAGTGCAG GGTGGGAGG GAAACGGCCT CTGCGGGAG AAGCAAGGGG CCCGCCTGGC	60
GGGGCGCAA GACCCGGAA GCCGCGCCGG GAGGAGGGTC GGGCGGGTCT CAGCCACTCC	120
TCGTCCCCAG	130

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 130 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 2403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

GTGAGTGCAG GGTGGGAGG GAAACGGCCT CTGCGGGAG AAGCAAGGGG CCCGCCTGGC	60
GGGGCGCAA GACCCGGAA GCCGCGCCGG GAGGAGGGTC GGGCGGGTCT CAGCCACTCC	120

TCGTCCCCAG

130

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 2404

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GTGAGTGCAG GGTGGGAGG GAAACGGCCT CTGCGGGAG AAGCAAGGGG CCCGCCTGGC GGGGGGCAA GACCCGGGAA GCCCGGCCGG GAGGAGGGTC GGGCGGGTCT CAGCCACTCC TCGTCCCCAG	60 120 130
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(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 2405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GTGAGTGCAG GGTGGGAGG GAAACGGCCT CTGCGGGAG AAGCAAGGGG CCCGCCTGGC GGGGGGCAA GACCCGGGAA GCCCGGCCGG GAGGAGGGTC GGGCGGGTCT CAGCCACTCC TCGTCCCCAG	60 120 130
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(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no

- (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 2407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

GTGAGTGCAG GGTCGGGAGG GAAACGGCCT CTGCGGGAG AAGCAAGGGG CCCGCCTGGC	60
GGGGCGCAA GACCCGGAA GCCGCGCCGG GAGGAGGGTC GGGCGGGTCT CAGCCACTCC	120
TCGTCCCCAG	130

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 129 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 2501

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

GTGAGTGCAG GGTCGTGGGG AAACCGCCTC TGCGGGGAGA AGCAAGGGGC CCGCCCGGCG	60
GGGACGCAGG ACCCGGGTAG CGCGGCCGGG AGGAGGGTCG GGTGGGTCTC AGCCACTCCT	120
CGCCCCCAG	129

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 130 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 2601

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

GTGAGTGCAG GGTCGGGAGG GAAACGGCCT CTGTGGGAG AAGCAAGGGG CCCGCCGGC	60
GGGGCGCAA GACCCGGAA GCCGCGCCTG GAGGAGGGTC GGGCGGGTCT CAGCCACTCC	120
TCGTCCCCAG	130

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 3402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

GTGAGTGCAG GGTGGGGAGG GAAACGGCCT CTGTGGGGAG AAGCAAGGGG CCCGCCGGC	60
GGGGGGCGCAG GACCCGGGAA GCCGCGCCTG GAGGAGGGTC GGGCGGGTCT CAGCCACTCC	120
TCGCCCCCAG	130

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 6601

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GTGAGTGCAG GGTGGGGAGG GAAACGGCCT CTGTGGGGAG AAGCAAGGGG CCCGCCGGC	60
GGGGGGCGCAG GACCCGGGAA GCCGCGCCTG GAGGAGGGTC GGGCGGGTCT CAGCCACTCC	120
TCGCCCCCAG	130

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human

(ix) FEATURE:

(A) NAME/KEY: HLA-A Intron 1 Allele A* 6602

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

GTGAGTGCAG GGTGGGAGG GAAACGGCCT CTGTGGGAG AAGCAAGGGG CCCGCCGGC	60
GGGGCGCAG GACCCGGAA GCCGCGCCTG GAGGAGGGTC GGGCGGGTCT CAGCCACTCC	120
TCGCCCCCAG	130

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 6603

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

GTGAGTGCAG GGTGGGAGG GAAACGGCCT CTGTGGGAG AAGCAAGGGG CCCGCCGGC	60
GGGGCGCAG GACCCGGAA GCCGCGCCTG GAGGAGGGTC GGGCGGGTCT CAGCCACTCC	120
TCGCCCCCAG	130

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 4301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

GTGAGTGCAG GGTGGGAGG GAAACGGCCT CTGTGGGAG AAGCAAGGGG CCCGCCGGC	60
GGGGCGCAG GACCCGGAA GCCGCGCCTG GAGGAGGGTC GGGCGGGTCT CAGCCACTCC	120
TCGCCCCCAG	130

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 2901

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

GTGAGTGCAGG GGTCTGGGG AAACCGCCTC TGCAGGGAGA AGCAAGGGGC CCGCCCGGCG	60
GGGACGCAGG ACCCGGGTAG CCGCGCCGGG AGGAGGGTCG GGTGGGTCTC AGCCACTCCT	120
CGCCCCCAG	129

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 2902

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

GTGAGTGCAGG GGTCTGGGG AAACCGCCTC TGCAGGGAGA AGCAAGGGGC CCGCCCGGCG	60
GGGACGCAGG ACCCGGGTAG CCGCGCCGGG AGGAGGGTCG GGTGGGTCTC AGCCACTCCT	120
CGCCCCCAG	129

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 3101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

GTGAGTGCAG	GGTCGTGGGG	AAACCGCCTC	TGCGGGGAGA	AGCAAGGGGC	CCGCCCGGCG	60
GGGGCGCAGG	ACCCGGGTAG	CCGCGCCGGG	AGGAGGGTCG	GGCGGATCTC	AGCCACTCCT	120
CGCCCCCAG						129

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 3201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

GTGAGTGCAG	GGTCGTGGGG	AAACCGCCTC	TGCGGGGAGA	AGCAAGGGGC	CCGCCCGGCG	60
GGGGCGCAGG	ACCCGGGTAG	CCGCGCCGGG	AGGAGGGTCG	GGCGGATCTC	AGCCACTCCT	120
CGCCCCCAG						129

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 3301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

GTGAGTGCAG	GGTCGTGGGG	AAACCGCCTC	TGCGGGGAGA	AGCAAGGGGC	CCGCCCGGCG	60
GGGGCGCAGG	ACCCGGGTAG	CCGCGCCGGG	AGGAGGGTCG	GGCGGATCTC	AGCCACTCCT	120
CGCCCCCAG						129

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 3303

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

GTGAGTGCAG GGTCTGGGG AAACCGCCTC TGCAGGGAGA AGCAAGGGGC CCGCCCGGCG	60
GGGGCGCAGG ACCCGGGTAG CCGCGCCGGG AGGAGGGTCG GGCGGATCTC AGCCACTCCT	120
CGCCCCCAG	129

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 129 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 7401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

GTGAGTGCAG GGTCTGGGG AAACCGCCTC TGCAGGGAGA AGCAAGGGGC CCGCCCGGCG	60
GGGGCGCAGG ACCCGGGTAG CCGCGCCGGG AGGAGGGTCG GGCGGATCTC AGCCACTCCT	120
CGCCCCCAG	129

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 129 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 7402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

GTGAGTGCAGG GGTCTGGGG AAACCGCCTC TGCAGGGAGA AGCAAGGGGC CCGCCCGGCG 60
 GGGGCGCAGG ACCCGGGTAG CCGCGCCGGG AGGAGGGTCG GGCGGGTCTC AGCCACTCCT 120
 CGCCCCCAG 129

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 7403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GTGAGTGCAGG GGTCTGGGG AAACCGCCTC TGCAGGGAGA AGCAAGGGGC TCGCCCGGCG 60
 GGGGCGCAGG ACCCGGGTAG CCGCGCCGGG AGGAGGGTCG GGCGGGTCTC AGCCACTCCT 120
 CGCCCCCAG 129

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 8001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

GTGAGTGCAGG GGTCTGGGGAGG GAAACGGCCT CTGCGGGGAG AAGCAAGGGG CCCGCCCGGC 60
 GGGGCGCAG GACCCGGGAA GCCGCGCCGG GAGGAGGGTC GGGCGGGTCT CAGCCACTCC 120
 TCGCCCCCAG 130

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA

- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele consensus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GTGAGTGACC CCGGCCCCGGG GCGCAGGTCA CGACCCCTCA TCCCCCACGG ACGGGCCAGG	60
TCGCCCACAG TCTCCGGGTC CGAGATCCAC CCCGAAGCCG CGGGACCCCG AGACCCTTGC	120
CCCAGGAGAG GCCCAGGGCGC CTTTACCCGG TTTCATTTTC AGTTTAGGCC AAAAATCCCC	180
CCGGGTTGGT CGGGGCCGGG CGGGGCTCGG GGGACTGGGC TGACCGCGGG GTCGGGGCCA	240
G	241

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 241 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 0101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GTGAGTGACC CCGGCCCCGGG GCGCAGGTCA CGACCCCTCA TCCCCCACGG ACGGGCCAGG	60
TCGCCCACAG TCTCCGGGTC CGAGATCCAC CCCGAAGCCG CGGGACTCCG AGACCCTTGT	120
CCCAGGAGAG GCCCAGGGCGC CTTTACCCGG TTTCATTTTC AGTTTAGGCC AAAAATCCCC	180
CCGGGTTGGT CGGGGCCGGG CGGGGCTCGG GGGACTGGGC TGACCGCGGG GTCGGGGCCA	240
G	241

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 241 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 0201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GTGAGTGACC CCGGCCCCGGG GCGCAGGTCA CGACCTCTCA TCCCCCACGG ACGGGCCAGG	60
TCGCCCACAG TCTCCGGGTC CGAGATCCGC CCCGAAGCCG CGGGACCCCG AGACCCTTGC	120
CCCAGGGAGAG GCCCAGGCAG CTTTACCCGG TTTCATTTTC AGTTTAGGCC AAAAATCCCC	180
CCAGGTTGGT CGGGGCGGGG CGGGGCTCGG GGGACCGGGC TGACCGCGGG GTCCGGGCCA	240
G	241

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron Allele A* 0202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

GTGAGTGACC CCGGCCCCGGG GCGCAGGTCA CGACCTCTCA TCCCCCACGG ACGGGCCAGG	60
TCGCCCACAG TCTCCGGGTC CGAGATCCGC CCCGAAGCCG CGGGACCCCG AGACCCTTGC	120
CCCAGGGAGAG GCCCAGGCAG CTTTACCCGG TTTCATTTTC AGTTTAGGCC AAAAATCCCC	180
CCAGGTTGGT CGGGGCGGGG CGGGGCTCGG GGGACCGGGC TGACCGCGGG GTCCGGGCCA	240
G	241

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron Allele A* 0203

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GTGAGTGACC CCGGCCCCGGG GCGCAGGTCA CGACCTCTCA TCCCCCACGG ACGGGCCAGG	60
TCGCCCACAG TCTCCGGGTC CGAGATCCGC CCCGAAGCCG CGGGACCCCG AGACCCTTGC	120
CCCAGGGAGAG GCCCAGGCAG CTTTACCCGG TTTCATTTTC AGTTTAGGCC AAAAATCCCC	180
CCAGGTTGGT CGGGGCGGGG CGGGGCTCGG GGGACCGGGC TGACCGCGGG GTCCGGGCCA	240
G	241

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 0204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

GTGAGTGACC CCGGCCCCGGG GCGCAGGTCA CGACCTCTCA TCCCCCACGG ACGGGCCAGG	60
TCGCCCACAG TCTCCGGGTC CGAGATCCGC CCCGAAGCCG CGGGACCCCG AGACCCCTTGC	120
CCCAGGAGAG GCCCAGGCGC CTTTACCCGG TTTCATTTC AGTTTAGGCC AAAAATCCCC	180
CCAGGTTGGT CGGGGCGGGG CGGGGCTCGG GGGACCGGGC TGACCGCGGG GTCCGGGCCA	240
G	241

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 0205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

GTGAGTGACC CCGGCCCCGGG GCGCAGGTCA CGACCTCTCA TCCCCCACGG ACGGGCCAGG	60
TCGCCCACAG TCTCCGGGTC CGAGATCCGC CCCGAAGCCG CGGGACCCCG AGACCCCTTGC	120
CCCAGGAGAG GCCCAGGCGC CTTTACCCGG TTTCATTTC AGTTTAGGCC AAAAATCCCC	180
CCAGGTTGGT CGGGGCGGGG CGGGGCTCGG GGGACCGGGC TGACCGCGGG GTCCGGGCCA	240
G	241

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: no
 (iv) ANTI-SENSE: no
 (v) ORIGINAL SOURCE:
 (A) ORGANISM: human
 (ix) FEATURE:
 (A) NAME/KEY: HLA-A Intron 2 Allele A* 0206

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

GTGAGTGACC CCGGCCCCGGG GCGCAGGTCA CGACCTCTCA TCCCCCACGG ACGGGCCAGG	60
TCGCCCCACAG TCTCCGGGTC CGAGATCCGC CCCGAAGCCG CGGGACCCCG AGACCCTTGC	120
CCCGGGAGAG GCCCAGGCGC CTTTACCCGG TTTCATTTC AGTTTAGGCC AAAAATCCCC	180
CCAGGTTGGT CGGGGCGGGG CGGGGCTCGG GGGACCGGGC TGACCGCGGG GTCCGGGCCA	240
G	241

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 241 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (iii) HYPOTHETICAL: no
 (iv) ANTI-SENSE: no
 (v) ORIGINAL SOURCE:
 (A) ORGANISM: human
 (ix) FEATURE:
 (A) NAME/KEY: HLA-A Intron 2 Allele A* 0207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GTGAGTGACC CCGGCCCCGGG GCGCAGGTCA CGACCTCTCA TCCCCCACGG ACGGGCCAGG	60
TCGCCCCACAG TCTCCGGGTC CGAGATCCGC CCCGAAGCCG CGGGACCCCG AGACCCTTGC	120
CCCGGGAGAG GCCCAGGCGC CTTTACCCGG TTTCATTTC AGTTTAGGCC AAAAATCCCC	180
CCAGGTTGGT CGGGGCGGGG CGGGGCTCGG GGGACCGGGC TGACCGCGGG GTCCGGGCCA	240
G	241

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 241 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (iii) HYPOTHETICAL: no
 (iv) ANTI-SENSE: no
 (v) ORIGINAL SOURCE:
 (A) ORGANISM: human
 (ix) FEATURE:
 (A) NAME/KEY: HLA-A Intron 2 Allele A* 0208

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GTGAGTGACC CCGGCCCCGGG GCGCAGGTCA CGACCTCTCA TCCCCCACGG ACGGGCCAGG	60
TCGCCCCACAG TCTCCGGGTC CGAGATCCGC CCCGAAGCCG CGGGACCCCG AGACCCTTGC	120
CCCAGGGAGAG GCCCAGGCGC CTTTACCCGG TTTCATTTTC AGTTTAGGCC AAAAATCCCC	180
CCAGGTTGGT CGGGGCGGGG CGGGGCTCGG GGGACCGGGC TGACCGCGGG GTCCGGGCCA	240
G	241

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 0209

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

GTGAGTGACC CCGGCCCCGGG GCGCAGGTCA CGACCTCTCA TCCCCCACGG ACGGGCCAGG	60
TCGCCCCACAG TCTCCGGGTC CGAGATCCGC CCCGAAGCCG CGGGACCCCG AGACCCTTGC	120
CCCAGGGAGAG GCCCAGGCGC CTTTACCCGG TTTCATTTTC AGTTTAGGCC AAAAATCCCC	180
CCAGGTTGGT CGGGGCGGGG CGGGGCTCGG GGGACCGGGC TGACCGCGGG GTCCGGGCCA	240
G	241

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 0210

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GTGAGTGACC CCGGCCCCGGG GCGCAGGTCA CGACCTCTCA TCCCCCACGG ACGGGCCAGG	60
TCGCCCCACAG TCTCCGGGTC CGAGATCCGC CCCGAAGCCG CGGGACCCCG AGACCCTTGC	120
CCCAGGGAGAG GCCCAGGCGC CTTTACCCGG TTTCATTTTC AGTTTAGGCC AAAAATCCCC	180
CCAGGTTGGT CGGGGCGGGG CGGGGCTCGG GGGACCGGGC TGACCGCGGG GTCCGGGCCA	240
G	241

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 0211

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GTGAGTGACC CCGGCCGGG GCGCAGGTCA CGACCTCTCA TCCCCCACGG ACGGGCCAGG	60
TCGCCCACAG TCTCCGGGTC CGAGATCCGC CCCGAAGCCG CGGGACCCCG AGACCCTTGC	120
CCCAGGAGAG GCCCAGGCGC CTTTACCCGG TTTCATTTC AGTTTAGGCC AAAAATCCCC	180
CCAGGTTGGT CGGGGCGGGG CGGGGCTCGG GGGACCGGGC TGACCGCGGG GTCCGGGCCA	240
G	241

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron Allele A* 0215

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

GTGAGTGACC CCGGCCGGG GCGCAGGTCA CGACCTCTCA TCCCCCACGG ACGGGCCAGG	60
TCGCCCACAG TCTCCGGGTC CGAGATCCGC CCCGAAGCCG CGGGACCCCG AGACCCTTGC	120
CCCAGGAGAG GCCCAGGCGC CTTTACCCGG TTTCATTTC AGTTTAGGCC AAAAATCCCC	180
CCAGGTTGGT CGGGGCGGGG CGGGGCTCGG GGGACCGGGC TGACCGCGGG GTCCGGGCCA	240
G	241

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA

- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 0217

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

GTGAGTGACC CCGGCCCCGGG GCGCAGGTCA CGACCTCTCA TCCCCCACGG ACGGGCCAGG	60
TCGCCCACAG TCTCCGGGTC CGAGATCCGC CCCGAAGCCG CGGGACCCCG AGACCCTTGC	120
CCCGGGAGAG GCCCAGGCGC CTTTACCCGG TTTCATTTC AGTTTAGGCC AAAAATCCCC	180
CCAGGTTGGT CGGGGCGGGG CGGGGCTCGG GGGACCGGGC TGACCGCGGG GTCCGGGCCA	240
G	241

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 241 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 6801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

GTGAGTGACC CCGGCCCCGGG GCGCAGGTCA CGACCCCTCA TCCCCCACGG ACGGGCCAGG	60
TCGCCCACAG TCTCCGGGTC CGAGATCCGC CCCGAAGCCG CGGGACCCCG AGACCCTTGC	120
CCCGGGAGAG GCCCAGGCGC CTTTACCCGG TTTCATTTC AGTTTAGGCC AAAAATCCCC	180
CCGGGTTGGT CGGGGCGGGG CGGGGCTCGG GGGACCGGGC TGACCTCGGG GTCCGGGCCA	240
G	241

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 241 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 6802

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GTGAGTGACC CCGGCCCCGGG GCGCAGGTCA CGACCCCTCA TCCCCCACGG ACGGGCCAGG	60
TCGCCCACAG TCTCCGGGTC CGAGATCCGC CCCGAAGCCG CGGGACCCCG AGACCCCTTGC	120
CCCAGGAGAG GCCCAGGCAG CTTTACCCGG TTTCATTTC AGTTTAGGCC AAAAATCCCC	180
CCGGGTTGGT CGGGGCGGGG CGGGGCTCGG GGGACCGGGC TGACCTCGGG GTCCGGGCCA	240
G	241

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 6901

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

GTGAGTGACC CCGGCCCCGGG GCGCAGGTCA CGACCTCTCA TCCCCCACGG ACGGGCCAGG	60
TCGCCCACAG TCTCCGGGTC CGAGATCCGC CCCGAAGCCG CGGGACCCCG AGACCCCTTGC	120
CCCAGGAGAG GCCCAGGCAG CTTTACCCGG TTTCATTTC AGTTTAGGCC AAAAATCCCC	180
CCAGGTTGGT CGGGGCGGGG CGGGGCTCGG GGGACCGGGC TGACCCGCGGG GTCCGGGCCA	240
G	241

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 2501

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GTGAGTGACC CCGGCCCCGGG GCGCAGGTCA CGACCCCTCA TCCCCCACGG ACGGGCCAGG	60
TCGCCCACAG TCTCCGGGTC CGAGATCCGC CCCGAAGCCG CGGGACCCCG AGACCCCTTGC	120
CCCAGGAGAG GCCCAGGCAG CTTTACCCGG TTTCATTTC AGTTTAGGCC AAAAATCCCC	180
CCGGGTTGGT CGGGGCGGGG CGGGGCTCGG GGGACCGGGC TGACCTCGGG GTCCGGGCCA	240
G	241

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 2601

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

GTGAGTGACC CCGGCCGGGG GCGCAGGTCA CGACCCCTCA TCCCCCACGG ACGGGCCAGG	60
TCGCCCACAG TCTCCGGGTC CGAGATCCGC CCCGAAGCCG CGGGACCCCG AGACCCTTGC	120
CCCAGGAGAG GCCCAGGCGC CTTTACCCGG TTTCATTTTC AGTTTAGGCC AAAAATCCCC	180
CGGGGTTGGT CGGGGCCGGGG CGGGGCTCGG GGGACCGGGC TGACCTCGGG GTCCGGGCA	240
G	241

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 4301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

GTGAGTGACC CCGGCCGGGG GCGCAGGTCA CGACCCCTCA TCCCCCACGG ACGGGCCAGG	60
TCGCCCACAG TCTCCGGGTC CGAGATCCGC CCCGAAGCCG CGGGACCCCG AGACCCTTGC	120
CCCAGGAGAG GCCCAGGCGC CTTTACCCGG TTTCATTTTC AGTTTAGGCC AAAAATCCCC	180
CGGGGTTGGT CGGGGCCGGGG CGGGGCTCGG GGGACCGGGC TGACCTCGGG GTCCGGGCA	240
G	241

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA

- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 6601

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

GTGAGTGACC CCGGCCCCGGG GCGCAGGTCA CGACCCCTCA TCCCCCACGG ACGGGCCAGG	60
TCGCCCACAG TCTCCGGGTC CGAGATCCGC CCCGAAGCCG CGGGACCCCG AGACCCTTGC	120
CCCGGGAGAG GCCCAGGCAG CTTTACCCGG TTTCATTTTC AGTTTAGGCC AAAAATCCCC	180
CCGGGTTGGT CGGGGCGGGG CGGGGCTCGG GGGACCGGGC TGACCTCGGG GTCCGGGCCA	240
G	241

(2) INFORMATION FOR SEQ ID NO:109:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 241 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 6602

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

GTGAGTGACC CCGGCCCCGGG GCGCAGGTCA CGACCCCTCA TCCCCCACGG ACGGGCCAGG	60
TCGCCCACAG TCTCCGGGTC CGAGATCCGC CCCGAAGCCG CGGGACCCCG AGACCCTTGC	120
CCCGGGAGAG GCCCAGGCAG CTTTACCCGG TTTCATTTTC AGTTTAGGCC AAAAATCCCC	180
CCGGGTTGGT CGGGGCGGGG CGGGGCTCGG GGGACCGGGC TGACCTCGGG GTCCGGGCCA	240
G	241

(2) INFORMATION FOR SEQ ID NO:110:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 241 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 6603

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

GTGAGTGACC CCGGCCCCGGG GCGCAGGTCA CGACCCCTCA TCCCCCACGG ACGGGCCAGG	60
TCGCCCACAG TCTCCGGGTC CGAGATCCGC CCCGAAGCCG CGGGACCCCG AGACCCTTGC	120
CCCAGGAGAG GCCCAGGCC CTTTACCCGG TTTCATTTTC AGTTTAGGCC AAAAATCCCC	180
CCGGGTTGGT CGGGGCGGGG CGGGGCTCGG GGGACCGGGC TGACCTCGGG GTCCGGGCCA	240
G	241

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 3402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

GTGAGTGACC CCGGCCCCGGG GCGCAGGTCA CGACCTCTCA TCCCCCACGG ACGGGCCGGG	60
TCGCCCACAG TCTCCGGGTC CGAGATCCAC CCCGAAGCCG CGGGACCCCG AGACCCTTGC	120
CCCAGGAGAG GCCCAGGCC CTTTACCCGG TTTCATTTTC AGTTTAGGCC AAAAATCCCC	180
CCGGGTTGGT CGGGGCGGGG CGGGGCTCGG GGGACCGGGC TGACCTCGGG GTCCGGGCCA	240
G	241

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 2901

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

GTGAGTGACC CCGGCCCCGGG GCGCAGGTCA CGACCTCTCA TCCCCCACGG ACGGGCCGGG	60
TCGCCCACAG TCTCCGGGTC CGAGATCCAC CCCGAAGCCG CGGGACCCCG AGACCCTTGC	120
CCCAGGAGAG GCCCAGGCC CTTTACCCGG TTTCATTTTC AGTTTAGGCC AAAAATCCCC	180
CCGGGTTGGT CGGGGCCCGA CGGGGCTCGG GGGACTGGGC TGACCGTGGG GTCCGGGCCA	240
G	241

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 2902

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

GTGAGTGACC CCGGCCCGGG GCGCAGGTCA CGACCTCTCA TCCCCCACGG ACGGGCCGGG	60
TCGCCCCACAG TCTCCGGGTC CGAGATCCAC CCCGAAGCCG CGGGACCCCG AGACCCTTGC	120
CCCAGGAGAG GCCCAGGCGC CTTTACCCGG TTTCAATTTC AGTTTAGGCC AAAAATCCCC	180
CCGGGTTGGT CGGGGCCGGA CGGGGCTCGG GGGACTGGGC TGACCGTGGG GTCGGGGCCA	240
G	241

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 3101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

GTGAGTGACC CCAGCCCGGG GCGCAGGTCA CGACCTCTCA TCCCCCACGG ACGGGCCAGG	60
TCACCCACAG TCTCCGGGTC CGAGATCCAC CCCGAAGCCG CGGGACCCCG AGACCCTTGC	120
CCCAGGAGAG GCCCAGGCGC CTTTACCCGG TTTCAATTTC AGTTTAGGCC AAAAATCCCC	180
CCGGGTTGGT CGGGGCCGGA CGGGGCTCGG GGGACTGGGC TGACCGTGGG GTCGGGGCCA	240
G	241

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA

- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 3201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

GTGAGTGACC CCGGCCCCGGG GCGCAGGTCA CGACCTCTCA TCCCCCACGG ACGGGCCAGG	60
TCGCCCCACAG TCTCCGGGTC CGAGATCCAC CCCGAAGCCG CGGGACCCCG AGACCCTTGC	120
CCCGGGAGAG GCCCAGGCGC CTTTACCCGG TTTCACTTTC AGTTTAGGCC AAAAATCCCC	180
CCGGGTTGGT CGGGGCCCGGA CGGGGCTCGG GGGACTGGGC TGACCGTGGG GTCGGGCCA	240
G	241

(2) INFORMATION FOR SEQ ID NO:116:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 241 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 3301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

GTGAGTGACC CCAGCCCCGGG GCGCAGGTCA CGACCTCTCA TCCCCCACGG ACGGGCCAGG	60
TCACCCACAG TCTCCGGGTC CGAGATCCAC CCCGAAGCCG CGGGACCCCG AGACCCTTGC	120
CCCGGGAGAG GCCCAGGCGC CTTTACCCGG TTTCACTTTC AGTTTAGGCC AAAAATCCCC	180
CCGGGTTGGT CGGGGCCCGGA CGGGGCTCGG GGGACTGGGC TGACCGTGGG GTCGGGCCA	240
G	241

(2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 241 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 3303

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

GTGAGTGACC CCAGCCGGG GCGCAGGTCA CGACCTCTCA TCCCCCACGG ACGGGCCAGG	60
TCACCCACAG TCTCCGGTC CGAGATCCAC CCCGAAGCCG CGGGACCCCG AGACCCTTGC	120
CCCAGGAGAG GCCCAGGCAC CTTTACCCGG TTTCATTTTC AGTTTAGGCC AAAAATCCCC	180
CCGGGTTGGT CGGGGCCGGA CGGGCTCGG GGGACTGGGC TGACCGTGGG GTCGGGGCCA	240
G	241

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (iii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 7401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

GTGAGTGACC CCGGCCGGGG GCGCAGGTCA GGACCCCTCA TCCCCCACGG ACGGGCCAGG	60
TCGCCCACAG TCTCCGGTC CGAGATCCAC CCCGAAGCCG CGGGACCCCG AGACCCTTGC	120
CCCAGGAGAG GCCCAGGCAC CTTTACCCGG TTTCATTTTC AGTTTAGGCC AAAAATCCCC	180
CCGGGTTGGT CGGGGCCGGA CGGGCTCGG GGGACTGGGC TGACCGTGGG GTCGGGGCCA	240
G	241

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (iii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 7402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

GTGAGTGACC CCGGCCGGGG GCGCAGGTCA CGACCTCTCA TCCCCCACGG ACGGGCCAGG	60
TCGCCCACAG TCTCCGGTC CGAGATCCAC CCCGAAGCCG CGGGACCCCG AGACCCTTGC	120
CCCAGGAGAG GCCCAGGCAC CTTTACCCGG TTTCATTTTC AGTTTAGGCC AAAAATCCCC	180
CCGGGTTGGT CGGGGCCGGA CGGGCTCGG GGGACTGGGC TGACCGTGGG GTCGGGGCCA	240
G	241

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 7403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

GTGAGTGACC CCGGCCGGGG GCGCAGGTCA GGACCCCTCA TCCCCCACGG ACGGGCCAGG	60
TCGCCCACAG TCTCCGGGTC CGAGATCCAC CCCGAAGCCG CGGGACCCCG AGACCCTTGC	120
CCCGGGAGAG GCCCAGGCGC CTTAACCCGG TTTCATTTC AGTTTAGGCC AAAAATCCCC	180
CCGGGTTGGT CGGGGCCGGA CGGGGCTCGG GGGACTGGGC TGACCGTGGG GTCGGGGCCA	240
G	241

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 2301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

GTGAGTGACC CCGGCCGGGG GCGCAGGTCA CGACCCCTCA TCCCCCACGG ACGGGCCGGG	60
TCGCCCACAG TCTCCGGGTC CGAGATCCAC CCCGAAGCCG CGGGACCCCG AGACCCTTGC	120
CCCGGGAGAG GCCCAGGCGC CTTAACCCGG TTTCATTTC AGTTTAGGCC AAAAATCCCC	180
CCGGGTTGGT CGGGGCCGGG CGGGGCTCGG GGGACTGGGC TGACCGCAGG GTCGGGGCCA	240
G	241

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: no
 (iv) ANTI-SENSE: no
 (v) ORIGINAL SOURCE:
 (A) ORGANISM: human
 (ix) FEATURE:
 (A) NAME/KEY: HLA-A Intron 2 Allele A* 2402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

GTGAGTGACC CCGGCCCGGG GCGCAGGTCA CGACCCCTCA TCCCCCACGG ACGGGCCGGG	60
TCGCCCACAG TCTCCGGGTC CGAGATCCAC CCCGAAGCCG CGGGACCCCG AGACCCTTGC	120
CCCAGGAGAG GCCCAGGCCG CTTAACCCGG TTTCATTTTC AGTTTAGGCC AAAAATCCCC	180
CCGGGTTGGT CGGGGCCGGG CGGGGCTCGG GGGACTGGC TGACCGCGGG GTCGGGGCCA	240
G	241

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 241 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (iii) HYPOTHETICAL: no
 (iv) ANTI-SENSE: no
 (v) ORIGINAL SOURCE:
 (A) ORGANISM: human
 (ix) FEATURE:
 (A) NAME/KEY: HLA-A Intron 2 Allele A* 2403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

GTGAGTGACC CCGGCCCGGG GCGCAGGTCA CGACCCCTCA TCCCCCACGG ACGGGCCGGG	60
TCGCCCACAG TCTCCGGGTC CGAGATCCAC CCCGAAGCCG CGGGACCCCG AGACCCTTGC	120
CCCAGGAGAG GCCCAGGCCG CTTAACCCGG TTTCATTTTC AGTTTAGGCC AAAAATCCCC	180
CCGGGTTGGT CGGGGCCGGG CGGGGCTCGG GGGACTGGC TGACCGCGGG GTCGGGGCCA	240
G	241

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 241 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (iii) HYPOTHETICAL: no
 (iv) ANTI-SENSE: no
 (v) ORIGINAL SOURCE:
 (A) ORGANISM: human
 (ix) FEATURE:
 (A) NAME/KEY: HLA-A Intron 2 Allele A* 2404

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

GTGAGTGACC CCGGCCCCGGG GCGCAGGTCA CGACCCCTCA TCCCCCACGG ACGGGCGGGG	60
TCGCCCACAG TCTCCGGGTC CGAGATCCAC CCCGAAGCCG CGGGACCCCG AGACCCTTGC	120
CCCAGGAGAG GCCCAGGCGC CTTAACCCGG TTTCATTTTC AGTTTAGGCC AAAAATCCCC	180
CCGGGTTGGT CGGGGCCGGG CGGGGCTCGG GGGACTGGGC TGACCGCGGG GTCGGGGCCA	240
G	241

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 2405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

GTGAGTGACC CCGGCCCCGGG GCGCAGGTCA CGACCCCTCA TCCCCCACGG ACGGGCGGGG	60
TCGCCCACAG TCTCCGGGTC CGAGATCCAC CCCGAAGCCG CGGGACCCCG AGACCCTTGC	120
CCCAGGAGAG GCCCAGGCGC CTTAACCCGG TTTCATTTTC AGTTTAGGCC AAAAATCCCC	180
CCGGGTTGGT CGGGGCCGGG CGGGGCTCGG GGGACTGGGC TGACCGCGGG GTCGGGGCCA	240
G	241

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 2407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

GTGAGTGACC CCGGCCCCGGG GCGCAGGTCA CGACCCCTCA TCCCCCACGG ACGGGCGGGG	60
TCGCCCACAG TCTCCGGGTC CGAGATCCAC CCCGAAGCCG CGGGACCCCG AGACCCTTGC	120
CCCAGGAGAG GCCCAGGCGC CTTAACCCGG TTTCATTTTC AGTTTAGGCC AAAAATCCCC	180
CCGGGTTGGT CGGGGCCGGG CGGGGCTCGG GGGACTGGGC TGACCGCGGG GTCGGGGCCA	240
G	241

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 0301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

GTGAGTGACC CCGGCCGGGG GCGCAGGTCA GGACCCCTCA TCCCCCACGG ACGGGCCAGG	60
TCGCCCACAG TCTCCGGGTC CGAGATCCAC CCCGAAGCCG CGGGACCCCG AGACCCTTGC	120
CCCAGGAGAG GCCCAGGCGC CTTTACCCGG TTTCATTTC AGTTTAGGCC AAAAATCCCC	180
CCGGGTTGGT CGGGGCTGGG CGGGCTCGG GGGACTGGGC TGACCGCGGG GTCGGGGCCA	240
G	241

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 1101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

GTGAGTGACC CCGGCCGGGG GCGCAGGTCA GGACCCCTCA TCCCCCACGG ACGGGCCAGG	60
TCGCCCACAG TCTCCGGGTC CGAGATCCAC CCCGAAGCCG CGGGACCCCG AGACCCTTGC	120
CCCAGGAGAG GCCCAGGCGC CTTTACCCGG TTTCATTTC AGTTTAGGCC AAAAATCCCC	180
CCGGGTTGGT CGGGGCTGGG CAGGGCTTGG GGGACTGGGC TGACCGCGGG GTCGGGGCCA	240
G	241

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA

- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 1102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

GTGAGTGACC CCGGCCGGGG GCGCAGGTCA CGACCCCTCA TCCCCCACGG ACGGGCCAGG	60
TGGCCACAG TCTCCGGGTC CGAGATCCAC CCCGAAGCCG CGGGACCCCG AGACCCCTGC	120
CCCAGGAGAG GCCCAGGCGC CTTTACCCGG TTTCATTTC AGTTTAGGCC AAAAATCCCC	180
CCGGGTTGGT CGGGGCCGGG CAGGGCTTGG GGGACTGGGC TGACCGCGGG GTCGGGGCCA	240
G	241

(2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 241 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 3001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

GTGAGTGACC CCGGCCGGGG GCGCAGGTCA CGACCCCTCA TCCCCCACGG ACGGGCCAGG	60
TCGCCACAG TCTCCGGGTC CGAGATCCAC CCCGAAGCCG CGGGACCCCG AGACCCCTGA	120
CCCAGGAGAG GCCCAGGCGC CTTTACCCGG TTTCATTTC AGTTTAGGCC AAAAATCCCC	180
CCGGGTTGGT CGGGGCTGGG CGGGGCTCGG GGGACTGGGC TGACCGCGGG GTCGGGGCCA	240
G	241

(2) INFORMATION FOR SEQ ID NO:131:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 241 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 3002

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

GTGAGTGACC CCGCCCGGGG GCGCAGGTCA CGACCCCTCA TCCCCCACGG ACGGGCCAGG	60
TCGCCCACAG TCTCCGGGTC CGAGATCCAC CCCGAAGCCG CGGGACCCCG AGACCCTTGA	120
CCCAGGAGAG GCCCAGGCGC CTTTACCCGG TTTCATTTC AGTTTAGGCC AAAAATTCCC	180
CCGGGTTGGT CGGGGCTGGG CGGGGCTCGG GGGACTGGGC TGACCGCGGG GTCGGGGCCA	240
G	241

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 3004

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

GTGAGTGACC CCGCCCGGGG GCGCAGGTCA CGACCCCTCA TCCCCCACGG ACGGGCCAGG	60
TCGCCCACAG TCTCCGGGTC CGAGATCCAC CCCGAAGCCG CGGGACCCCG AGACCCTTGA	120
CCCAGGAGAG GCCCAGGCGC CTTTACCCGG TTTCATTTC AGTTTAGGCC AAAAATTCCC	180
CCGGGTTGGT CGGGGCTGGG CGGGGCTCGG GGGACTGGGC TGACCGCGGG GTCGGGGCCA	240
G	241

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 8001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

GTGAGTGACC CCGCCCGGGG CGCAGGTCAC GACCCCTCAT CCCCTACGG ACGGCCAGGT	60
CGCCCACAGT CTCCGGGTCC GAGATCCACC CCCGAAGCCGC GGGACCCCGA GACCCCTGCC	120
CCCAGGAGAGG CCCAGGCGCC TTTAGCCGGT TTCATTTCGA GTTTAGGCCA AAAATCCCCC	180
CGGGTGGGTC GGGGCGGGGGC GGGGCTCGGG GGACCGGGCT GACCGCGGGG TCGGGGCCAG	240

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 602 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele consensus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

GTACCAGGGG CCACGGGGCG CCTCCCTGAT CGCCTGTAGA TCTCCCGGGC TGGCCTCCCA	60
CAAGGAGGGG AGACAATTGG GACCAACACT AGAATATCGC CCTCCCTCTG GTCCTGAGGG	120
AGAGGAATCC TCCTGGTTT CCAGATCCTG TACCAGAGAG TGACTCTGAG GTTCCGCCCT	180
GCTCTCTGAG CACAATTAAG GGATAAAAAT CTCTGAAGGA ATGACGGGAA GACGATCCCT	240
CGAATACTGA TGAGTGGTTC CCTTTGACAC ACACCGGCAG CAGCCTTGGG CCCGTGACTT	300
TTCCTCTCAG GCCTTGTCT CTGCTTCACA CTCAATGTGT GTGGGGGTCT GAGTCCAGCA	360
CTTCTGAGTC CCTCAGCCTC CACTCAGGTC AGGACCAGAA GTCGCTGTTC CCTCTTCAGG	420
GACTAGAATT TTCCACGGAA TAGGAGATTA TCCCAGGTGC CTGTGTCCAG GCTGGTGTCT	480
GGGTTCTGTG CTCCCTTCCC CATCCCAGGT GTCCCTGTCCA TTCTCAAGAT AGCCACATGT	540
GTGCTGGAGG AGTGTCCCAT GACAGATGCA AAATGCCTGA ATGTTCTGAC TCTTCCTGAC	600
AG	602

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 0101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

GTACCAGGGG CCACGGGGCG CCTCCCTGAT CGCCTATAGA TCTCCCGGGC TGGCCTCCCA	60
CAAGGAGGGG AGACAATTGG GACCAACACT AGAATATCAC CCTCCCTCTG GTCCTGAGGG	120
AGAGGAATCC TCCTGGTTT CCAGATCCTG TACCAGAGAG TGACTCTGAG GTTCCGCCCT	180
GCTCTCTGAG CACAATTAAG GGATAAAAATC TCTGAAGGAG TGACGGGAAG ACGATCCCTC	240
GAATACTGAT GAGTGGTTC CTTTGACACC GGCAGCAGCC TTGGGCCGT GACTTTCCCT	300
CTCAGGCCTT GTTCTCTGCT TCACACTCAA TGTGTGTGGG GGTCTGAGTC CAGCACCTCT	360
GAGTCTCTCA GCCTCCACTC AGGTCAAGGAC CAGAAGTCGC TGTCCCTTC TCAGGGAATA	420
GAAGATTATC CCAGGTGCCT GTGTCCAGGC TGGTGTCTGG GTTCTGTGCT CTCTTCCCCA	480

TCCCCGGGTGT CCTGTCCATT CTCAAGATGG CCACATGCGT GCTGGTGGAG TGTCCCATGA	540
CAGATGCAAA ATGCCTGAAT TTTCTGACTC TTCCCGTCAG	580

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 0301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

GTACCAGGGG CCACGGGGCG CCTCCCTGAT CGCCTGTAGA TCTCCCGGGC TGGCCTCCCA	60
CAAGGAGGGG AGACAATTGG GACCAACACT AGAATATCAC CCTCCCTCTG GTCTGAGGG	120
AGAGGAATCC TCCTGGGTTTC CAGATCCTGT ACCAGAGAGT GACTCTGAGG TTCCGCCCTG	180
CTCTCTGAGC ACAATTAAAGG GATAAAATCT CTGAAGGAGT GACGGGAAGA CGATCCCTCG	240
AATACTGATG AGTGGTTCCTC TTTGACACCG GCAGCAGCCT TGGGCCCCGTG ACTTTTCCTC	300
TCAGGCCTTG TTCTCTGCTT CACACTCAAT GTGTGTGGGG GTCTGAGTCC AGCACTTCTG	360
AGTCCCTCAG CCTCCACTCA GGTCAGGACC AGAAGTCGCT GTTCCCTTCT CAGGGAATAG	420
AAGATTATCC CAGGTGCCTG TGTCCAGGCT GGTGTCTGGG TTCTGTGCTC TCTTCCCCAT	480
CCCGGGTGTC CTGTCCATTTC TCAAGATGGC CACATGCGTG CTGGTGGAGT GTCCCATGAC	540
AGATGCAAAA TGCCTGAATT TTCTGACTCT TCCCCTCAG	579

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 1101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

GTACCAGGGG CCACGGGGCG CCTCCCTGAT CGCCTATAGA TCTCCCGGGC TGGCCTCCCA	60
CAAGGAGGGG AGACAATTGG GACCAACACT AGAATATCAC CCTCCCTCTG GTCTGAGGG	120
AGAGGAATCC TCCTGGGTTTC CCAGATCCTG TACCAGAGAG TGACTCTGAG GTTCCGCCCT	180
GCTCTCTGAG CACAATTAAAG GGATAAAATC TCTGAAGGAG TGACGGGAAG ACGATCCCTC	240
GAATACTGAT GAGTGGTTCCTC CTTTGACACC GGCAGCAGCC TTGGGCCCCGT GACTTTCCCT	300
CTCAGGCCTT GTTCTCTGCTT TCACACTCAA TGTGTGTGGG GGTCTGAGTC CAGCACTTCT	360

GAGTCTCTCA	GCCTCCACTC	AGGTCAAGGAC	CAGAAGTCGC	TGTTCCCTTC	TCAGGGAATA	420
GAAGATTATC	CCAGGTGCCT	GTGTCCAGGC	TGGTGTCTGG	GTTCTGTGCT	CTCTTCCCCA	480
TCCCAGGTGT	CCTGTCCATT	CTCAAGATGG	CCACATGCGT	GCTGGTGGAG	TGTCCCATGA	540
CAGATGCAAA	ATGCCTGAAT	TTTCTGACTC	TTCCCGTCAG			580

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 1102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

GTACCAGGGG	CCACGGGGCG	CCTCCCTGAT	CGCCTATAGA	TCTCCGGGC	TGGCCTCCCA	60
CAAGGAGGGG	AGACAATTGG	GACCAACACT	AGAATATCAC	CCTCCCTCTG	GTCCTGAGGG	120
AGAGGAATCC	TCCTGGTTT	CCAGATCCTG	TACCAGAGAG	TGACTCTGAG	GTTCCGCCCT	180
GCTCTCTGAG	CACAATTAAG	GGATAAAATC	TCTGAAGGAG	TGACGGGAAG	ACGATCCCTC	240
GAATACTGAT	GAGTGGTTCC	CTTGACACC	GGCAGCAGCC	TTGGGCCGT	GACTTTCCCT	300
CTCAGGCCCT	GTTCTCTGCT	TCACACTCAA	TGTGTGTGGG	GGTCTGAGTC	CAGCACTTCT	360
GAGTCTCTCA	GCCTCCACTC	AGGTCAAGGAC	CAGAAGTCGC	TGTTCCCTTC	TCAGGGAATA	420
GAAGATTATC	CCAGGTGCCT	GTGTCCAGGC	TGGTGTCTGG	GTTCTGTGCT	CTCTTCCCCA	480
TCCCAGGTGT	CCTGTCCATT	CTCAAGATGG	CCACATGCGT	GCTGGTGGAG	TGTCCCATGA	540
CAGATGCAAA	ATGCCTGAAT	TTTCTGACTC	TTCCCGTCAG			580

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 3001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

GTACCAGGGG	CCACGGGGCG	CCTCCCTGAT	CGCCTGTAGA	TCTCCGGGC	TGGCCTCCCA	60
CAAGGAGGGG	AGACAATTGG	GACCAACACT	AGAATATCAC	CCTCCCTCTG	GTCCTGAGGG	120
AGAGGAATCC	TCCTGGTTT	CCAGATCCTG	TACCAGAGAG	TGACTCTGAG	GTTCCGCCCT	180
GCTCTCTGAG	CACAATTAAG	GGATAAAATC	TCTGAAGGAG	TGACGGGAAG	ACGATCCCTC	240

GAATACTGAT GAGTGGTTCC CTTTGACACC GGCAGCAGCC TTGGGCCCGT GACTTTCCCT	300
CTCAGGCCCTT GTTCTCTGCT TCACACTCAA TGTGTGAGGG GGTCTGAGTC CAGCACTTCT	360
GAGTCCCTCA GCCTCCACTC AGGTCAAGGAC CAGAAGTCGC TGTTCCCTTC TCAGGGAATA	420
GAAGATTATC CCAGGTGCCT GTGTCCAGGC TGTTGTCTGG GTTCTGTGCT CTCTTCCCA	480
TCCCAGGTGT CCTGTCCATT CTCAAGATGG CCACATGCGT GCTGGTGGAG TGTCCCATGA	540
CAGATGCAAA ATGCCTGAAT TTTCTGACTC TTCCCGTCAG	580

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 3002

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

GTACCAGGGG CCACGGGGCG CCTTCCTGAT CGCCTGTAGA TCTCCGGGC TGGCCTCCCA	60
CAAGGAGGGG AGACAATTGG GACCAACACT AGAATATCAC CCTCCCTCTG GTCCTGAGGG	120
AGAGGAATCC TCCTGGGTTT CCAGATCCTG TACCAGAGAG TGACTCTGAG GTTCCGCCCT	180
GCTCTCTGAG CTCAATTAAAG GGATAAAAATC TCTGAAGGGAG TGACGGGAAG ACGATCCCTC	240
GAATACTGAT GAGTGGTTCC CTTTGACACC GGCAGCAGCC TTGGGCCCGT GACTTTCCCT	300
CTCAGGCCCTT GTTCTCTGCT TCACACTCAA TGTGTGAGGG GGTCTGAGTC CAGCACTTCT	360
GAGTCCCTCA GCCTCCACTC AGGTCAAGGAC CAGAAGTCGC TGTTCCCTTC TCAGGGAATA	420
GAAGATTATC CCAGGTGCCT GTGTCCAGGC TGTTGTCTGG GTTCTGTGCT CTCTTCCCA	480
TCCCAGGTGT CCTGTCCATT CTCAAGATGG CCACATGCGT GCTGGTGGAG TGTCCCATGA	540
CAGATGCAAA ATGCCTGAAT TTTCTGACTC TTCCCGTCAG	580

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 3004

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

GTACCAGGGG CCACGGGGCG CCTTCCTGAT CGCCTGTAGA TCTCCGGGC TGGCCTCCCA	60
CAAGGAGGGG AGACAATTGG GACCAACACT AGAATATCAC CCTCCCTCTG GTCCTGAGGG	120

100

AGAGGAATCC TCCTGGGTTT CCAGATCCTG TACCAGAGAG TGACTCTGAG GTTCCGCCCT	180
GCTCTCTGAG CACAATTAAG GGATAAAAATC TCTGAAGGAG TGACGGGAAG ACGATCCCTC	240
GAATACTGAT GAGTGGTTC CTTTGACACC GGCAGCAGCC TTGGGCCCGT GACTTTCCCT	300
CTCAGGCCCTT GTTCTCTGCT TCACACTCAA TGTGTGTGGG GGTCTGAGTC CAGCACTTCT	360
GAGTCCCTCA GCCTCCACTC AGGTCAAGGAC CAGAAGTCGC TGTTCCCTTC TCAGGGAATA	420
GAAGATTATC CCAGGTGCCT GTGTCCAGGC TGGTGTCTGG GTTCTGTGCT CTCTTCCCCA	480
TCCCGGGTGT CCTGTCCATT CTCAAGATGG CCACATGCGT GCTGGTGGAG TGTCCCAGTA	540
CAGATGCAAA ATGCCTGAAT TTTCTGACTC TTCCCGTCAG	580

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 0201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

GTACCAGGGG CCACGGGGCG CCTCCCTGAT CGCCTGTAGA TCTCCGGGC TGGCCTCCCA	60
CAAGGAGGGG AGACAATTGG GACCAACACT AGAATATTCGC CCTCCCTCTG GTCTGAGGG	120
AGAGGAATCC TCCTGGGTTT CCAGATCCTG TACCAGAGAG TGACTCTGAG GTTCCGCCCT	180
GCTCTCTGAG CACAATTAAG GGATAAAAATC TCTGAAGGAA TGACGGGAAG ACGATCCCTC	240
GAATACTGAT GAGTGGTTC CTTTGACACA CACAGGCAGC AGCCTTGGGC CCGTGACTTT	300
TCCTCTCAGG CCTTGTCTC TGCTTCACAC TCAATGTGTG TGGGGGTCTG AGTCCAGCAC	360
TTCTGAGTCC TTCAGCCTCC ACTCAGGTCA GGACCAGAAG TCGCTGTTCC CTCTTCAGGG	420
ACTAGAATTTC TCCACGGAAT AGGAGATTAT CCCAGGTGCC TGTGTCCAGG CTGGTGTCTG	480
GGTTCTGTGC TCCCTTCCCCC ATCCCAGGTG TCCTGTCCAT TCTCAAGATA GCCACATGTG	540
TGCTGGAGGA GTGTCCCAGTA ACAGATGCAA AATGCCTGAA TGATCTGACT CTTCCCTGACA	600
G	601

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 0202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

GTACCAGGGG CCACGGGGCG CCTCCCTGAT CGCCTGTAGA TCTCCCGGGC TGGCCTCCCA	60
CAAGGAGGGG AGACAATTGG GACCAACACT AGAATATCGC CCTCCCTCTG GTCCTGAGGG	120
AGAGGAATCC TCTGGGTTT CCAGATCCTG TACCAGAGAG TGACTCTGAG GTTCCGCCCT	180
GCTCTCTGAG CACAATTAAG GGATAAAATC TCTGAAGGAA TGACGGGAAG ACGATCCCTC	240
GAATACTGAT GAGTGGTTC CTTTGACACA CACAGGCAGC AGCCTTGGGC CGGTGACTTT	300
TCCTCTCAGG CCTTGTCTC TGCTTCACAC TCAATGTGTG TGGGGGTCTG AGTCCAGCAC	360
TTCTGAGTCC TTCAGCCTCC ACTCAGGTCA GGACCAGAAG TCGCTGTTCC CTCTTCAGGG	420
ACTAGAATT TCCACGGAAT AGGAGATTAT CCCAGGTGCC TGTGTCCAGG CTGGTGTCTG	480
GGTTCTGTGC TCCCTTCCCCC ATCCCAGGTG TCCTGTCCAT TCTCAAGATA GCCACATGTG	540
TGCTGGAGGA GTGTCCCAG ACAGATGCAA AATGCCTGAA TGATCTGACT CTTCCCTGACA	600
G	601

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 0203

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

GTACCAGGGG CCACGGGGCG CCTCCCTGAT CGCCTGTAGA TCTCCCGGGC TGGCCTCCCA	60
CAAGGAGGGG AGACAATTGG GACCAACACT AGAATATCGC CCTCCCTCTG GTCCTGAGGG	120
AGAGGAATCC TCTGGGTTT CCAGATCCTG TACCAGAGAG TGACTCTGAG GTTCCGCCCT	180
GCTCTCTGAG CACAATTAAG GGATAAAATC TCTGAAGGAA TGACGGGAAG ACGATCCCTC	240
GAATACTGAT GAGTGGTTC CTTTGACACA CACAGGCAGC AGCCTTGGGC CGGTGACTTT	300
TCCTCTCAGG CCTTGTCTC TGCTTCACAC TCAATGTGTG TGGGGGTCTG AGTCCAGCAC	360
TTCTGAGTCC TTCAGCCTCC ACTCAGGTCA GGACCAGAAG TCGCTGTTCC CTCTTCAGGG	420
ACTAGAATT TCCACGGAAT AGGAGATTAT CCCAGGTGCC TGTGTCCAGG CTGGTGTCTG	480
GGTTCTGTGC TCCCTTCCCCC ATCCCAGGTG TCCTGTCCAT TCTCAAGATA GCCACATGTG	540
TGCTGGAGGA GTGTCCCAG ACAGATGCAA AATGCCTGAA TGATCTGACT CTTCCCTGACA	600
G	601

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 0204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

GTACCAGGGG	CCACGGGGCG	CCTCCCTGAT	CGCCTGTAGA	TCTCCCGGGC	TGGCCTCCCA	60
CAAGGAGGGG	AGACAATTGG	GACCAACACT	AGAATATCGC	CCTCCCTCTG	GTCCTGAGGG	120
AGAGGAATCC	TCCTGGGTTT	CCAGATCCTG	TACCAGAGAG	TGACTCTGAG	GTTCCGCCCT	180
GCTCTCTGAG	CACAATTAAG	GGATAAAATC	TCTGAAGGAA	TGACGGGAAG	ACGATCCCTC	240
GAATACTGAT	GAGTGGTTCC	CTTTGACACA	CACAGGCAGC	AGCCTTGGGC	CCGTGACTTT	300
TCCTCTCAGG	CCTTGTTCCTC	TGCTTCACAC	TCAATGTGTG	TGGGGGTCTG	AGTCCAGCAC	360
TTCTGAGTCC	TTCAGCCTCC	ACTCAGGTCA	GGACCAGAAG	TCGCTGTTCC	CTCTTCAGGG	420
ACTAGAATT	TCCACGGAAT	AGGAGATTAT	CCCAGGTGCC	TGTGTCCAGG	CTGGTGTCTG	480
GGTTCTGTGC	TCCCTTCCCC	ATCCCAGGTG	TCCTGTCCAT	TCTCAAGATA	GCCACATGTG	540
TGCTGGAGGA	GTGTCCCATG	ACAGATGCAA	AATGCCTGAA	TGATCTGACT	CTTCCTGACA	600
G						601

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 0205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

GTACCAGGGG	CCACGGGGCG	CCTCCCTGAT	CGCCTGTAGA	TCTCCCGGGC	TGGCCTCCCA	60
CAAGGAGGGG	AGACAATTGG	GACCAACACT	AGAATATCGC	CCTCCCTCTG	GTCCTGAGGG	120
AGAGGAATCC	TCCTGGGTTT	CCAGATCCTG	TACCAGAGAG	TGACTCTGAG	GTTCCGCCCT	180
GCTCTCTGAG	CACAATTAAG	GGATAAAATC	TCTGAAGGAA	TGACGGGAAG	ACGATCCCTC	240
GAATACTGAT	GAGTGGTTCC	CTTTGACACA	CACAGGCAGC	AGCCTTGGGC	CCGTGACTTT	300
TCCTCTCAGG	CCTTGTTCCTC	TGCTTCACAC	TCAATGTGTG	TGGGGGTCTG	AGTCCAGCAC	360
TTCTGAGTCC	TTCAGCCTCC	ACTCAGGTCA	GGACCAGAAG	TCGCTGTTCC	CTCTTCAGGG	420
ACTAGAATT	TCCACGGAAT	AGGAGATTAT	CCCAGGTGCC	TGTGTCCAGG	CTGGTGTCTG	480
GGTTCTGTGC	TCCCTTCCCC	ATCCCAGGTG	TCCTGTCCAT	TCTCAAGATA	GCCACATGTG	540
TGCTGGAGGA	GTGTCCCATG	ACAGATGCAA	AATGCCTGAA	TGATCTGACT	CTTCCTGACA	600
G						601

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no

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(v) ORIGINAL SOURCE:
 (A) ORGANISM: human
 (ix) FEATURE:
 (A) NAME/KEY: HLA-A Intron 3 Allele A* 0206

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

GTACCAGGGG	CCACGGGGCG	CCTCCCTGAT	CGCCTGTAGA	TCTCCCGGGC	TGGCCTCCCA	60
CAAGGAGGGG	AGACAATTGG	GACCAACACT	AGAATATCGC	CCTCCCTCTG	GTCCTGAGGG	120
AGAGGAATCC	TCCTGGGTTT	CCAGATCCTG	TACCAGAGAG	TGACTCTGAG	GTTCCGCCCT	180
GCTCTCTGAG	CACAATTAAAG	GGATAAAATC	TCTGAAGGAA	TGACGGGAAG	ACGATCCCTC	240
GAATACTGAT	GAGTGGTTCC	CTTTGACACA	CACAGGCAGC	AGCCTTGGGC	CCGTGACTTT	300
TCCTCTCAGG	CCTTGTTCCTC	TGCTTCACAC	TCAATGTGTG	TGGGGGTCTG	AGTCCAGCAC	360
TTCTGAGTCC	TTCAGCCTCC	ACTCAGGTCA	GGACCAGAAG	TCGCTGTTCC	CTCTTCAGGG	420
ACTAGAATT	TCCACGGAAT	AGGAGATTAT	CCCAGGTGCC	TGTGTCCAGG	CTGGTGTCTG	480
GGTTCTGTGC	TCCCTTCCCC	ATCCCAGGTG	TCCTGTCCAT	TCTCAAGATA	GCCACATGTG	540
TGCTGGAGGA	GTGTCCCCATG	ACAGATGCAA	AATGCCTGAA	TGATCTGACT	CTTCCTGACA	600
G						601

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 601 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (iii) HYPOTHETICAL: no
 (iv) ANTI-SENSE: no
 (v) ORIGINAL SOURCE:
 (A) ORGANISM: human
 (ix) FEATURE:
 (A) NAME/KEY: HLA-A Intron 3 Allele A* 0207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

GTACCAGGGG	CCACGGGGCG	CCTCCCTGAT	CGCCTGTAGA	TCTCCCGGGC	TGGCCTCCCA	60
CAAGGAGGGG	AGACAATTGG	GACCAACACT	AGAATATCGC	CCTCCCTCTG	GTCCTGAGGG	120
AGAGGAATCC	TCCTGGGTTT	CCAGATCCTG	TACCAGAGAG	TGACTCTGAG	GTTCCGCCCT	180
GCTCTCTGAG	CACAATTAAAG	GGATAAAATC	TCTGAAGGAA	TGACGGGAAG	ACGATCCCTC	240
GAATACTGAT	GAGTGGTTCC	CTTTGACACA	CACAGGCAGC	AGCCTTGGGC	CCGTGACTTT	300
TCCTCTCAGG	CCTTGTTCCTC	TGCTTCACAC	TCAATGTGTG	TGGGGGTCTG	AGTCCAGCAC	360
TTCTGAGTCC	TTCAGCCTCC	ACTCAGGTCA	GGACCAGAAG	TCGCTGTTCC	CTCTTCAGGG	420
ACTAGAATT	TCCACGGAAT	AGGAGATTAT	CCCAGGTGCC	TGTGTCCAGG	CTGGTGTCTG	480
GGTTCTGTGC	TCCCTTCCCC	ATCCCAGGTG	TCCTGTCCAT	TCTCAAGATA	GCCACATGTG	540
TGCTGGAGGA	GTGTCCCCATG	ACAGATGCAA	AATGCCTGAA	TGATCTGACT	CTTCCTGACA	600
G						601

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 601 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA
 (iii) HYPOTHETICAL: no
 (iv) ANTI-SENSE: no
 (v) ORIGINAL SOURCE:
 (A) ORGANISM: human
 (ix) FEATURE:
 (A) NAME/KEY: HLA-A Intron 3 Allele A* 0208

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

GTACCAGGGG CCACGGGGCG CCTCCCTGAT CGCCTGTAGA TCTCCCGGGC TGGCCTCCCA	60
CAAGGAGGGG AGACAATTGG GACCAACACT AGAATATTCGC CCTCCCTCTG GTCCTGAGGG	120
AGAGGAATCC TCCTGGGTTT CCAGATCCTG TACCAGAGAG TGACTCTGAG GTTCCGCCCT	180
GCTCTCTGAG CACAATTAAAG GGATAAAAATC TCTGAAGGAA TGACGGGAAG ACGATCCCTC	240
GAATACTGAT GAGTGGTTCC CTTTGACACA CACAGGCAGC AGCCTTGGGC CCGTGACTTT	300
TCCTCTCAGG CCTTGTTCCTC TGCTTCACAC TCAATGTGTG TGGGGGTCTG AGTCCAGCAC	360
TTCTGAGTCC TTCAGCCTCC ACTCAGGTCA GGACCAGAAG TCGCTGTTCC CTCTTCAGGG	420
ACTAGAATTTC TCCACGGAAT AGGAGATTAT CCCAGGTGCC TGTGTCCAGG CTGGTGTCTG	480
GGTTCTGTGC TCCCTTCCCC ATCCCAGGTG TCCTGTCCAT TCTCAAGATA GCCACATGTG	540
TGCTGGAGGA GTGTCCCATG ACAGATGCAA AATGCCTGAA TGATCTGACT CTTCCGTACA	600
G	601

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 601 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (iii) HYPOTHETICAL: no
 (iv) ANTI-SENSE: no
 (v) ORIGINAL SOURCE:
 (A) ORGANISM: human
 (ix) FEATURE:
 (A) NAME/KEY: HLA-A Intron 3 Allele A* 0209

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

GTACCAGGGG CCACGGGGCG CCTCCCTGAT CGCCTGTAGA TCTCCCGGGC TGGCCTCCCA	60
CAAGGAGGGG AGACAATTGG GACCAACACT AGAATATTCGC CCTCCCTCTG GTCCTGAGGG	120
AGAGGAATCC TCCTGGGTTT CCAGATCCTG TACCAGAGAG TGACTCTGAG GTTCCGCCCT	180
GCTCTCTGAG CACAATTAAAG GGATAAAAATC TCTGAAGGAA TGACGGGAAG ACGATCCCTC	240
GAATACTGAT GAGTGGTTCC CTTTGACACA CACAGGCAGC AGCCTTGGGC CCGTGACTTT	300
TCCTCTCAGG CCTTGTTCCTC TGCTTCACAC TCAATGTGTG TGGGGGTCTG AGTCCAGCAC	360
TTCTGAGTCC TTCAGCCTCC ACTCAGGTCA GGACCAGAAG TCGCTGTTCC CTCTTCAGGG	420
ACTAGAATTTC TCCACGGAAT AGGAGATTAT CCCAGGTGCC TGTGTCCAGG CTGGTGTCTG	480
GGTTCTGTGC TCCCTTCCCC ATCCCAGGTG TCCTGTCCAT TCTCAAGATA GCCACATGTG	540
TGCTGGAGGA GTGTCCCATG ACAGATGCAA AATGCCTGAA TGATCTGACT CTTCCGTACA	600
G	601

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 0210

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

GTACCAGGGG CCACGGGGCG CCTCCCTGAT CGCCTGTAGA TCTCCCGGGC TGGCCTCCCA	60
CAAGGAGGGG AGACAATTGG GACCAACACT AGAATATTCG CCTCCCTCTG GTCCTGAGGG	120
AGAGGAATCC TCCTGGGTTT CCAGATCCTG TACCAGAGAG TGACTCTGAG GTTCCGCCCT	180
GCTCTCTGAG CACAATTAAG GGATAAAATC TCTGAAGGAA TGACGGGAAG ACGATCCCTC	240
GAATACTGAT GAGTGGTTCC CTTTGACACA CACAGGCAGC AGCCTGGGC CCGTGACTTT	300
TCCTCTCAGG CCTTGTTCCTC TGCTTCACAC TCAATGTGTG TGGGGGTCTG AGTCCAGCAC	360
TTCTGAGTCC TTCAGCCTCC ACTCAGGTCA GGACCAGAAG TCGCTGTTCC CTCTTCAGGG	420
ACTAGAATTT TCCACGGAAT AGGAGATTAT CCCAGGTGCC TGTGTCCAGG CTGGTGTCTG	480
GGTTCTGTGC TCCCTTCCCCC ATCCCAGGTG TCCTGTCCAT TCTCAAGATA GCCACATGTG	540
TGCTGGAGGA GTGTCCCAGT ACAGATGCAA AATGCCTGAA TGATCTGACT CTTCCCTGACA	600
G	601

(2) INFORMATION FOR SEQ ID NO:152:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 601 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 0211

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

GTACCAGGGG CCACGGGGCG CCTCCCTGAT CGCCTGTAGA TCTCCCGGGC TGGCCTCCCA	60
CAAGGAGGGG AGACAATTGG GACCAACACT AGAATATTCG CCTCCCTCTG GTCCTGAGGG	120
AGAGGAATCC TCCTGGGTTT CCAGATCCTG TACCAGAGAG TGACTCTGAG GTTCCGCCCT	180
GCTCTCTGAG CACAATTAAG GGATAAAATC TCTGAAGGAA TGACGGGAAG ACGATCCCTC	240
GAATACTGAT GAGTGGTTCC CTTTGACACA CACAGGCAGC AGCCTGGGC CCGTGACTTT	300
TCCTCTCAGG CCTTGTTCCTC TGCTTCACAC TCAATGTGTG TGGGGGTCTG AGTCCAGCAC	360
TTCTGAGTCC TTCAGCCTCC ACTCAGGTCA GGACCAGAAG TCGCTGTTCC CTCTTCAGGG	420
ACTAGAATTT TCCACGGAAT AGGAGATTAT CCCAGGTGCC TGTGTCCAGG CTGGTGTCTG	480
GGTTCTGTGC TCCCTTCCCCC ATCCCAGGTG TCCTGTCCAT TCTCAAGATA GCCACATGTG	540
TGCTGGAGGA GTGTCCCAGT ACAGATGCAA AATGCCTGAA TGATCTGACT CTTCCCTGACA	600
G	601

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 601 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(v) ORIGINAL SOURCE:

(A) ORGANISM: human

(ix) FEATURE:

(A) NAME/KEY: HLA-A Intron 3 Allele A* 0215

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

GTACCAGGGG CCACGGGGCG CCTCCCTGAT CGCCTGAGA TCTCCGGGC TGGCCTCCCA	60
CAAGGAGGGG AGACAATTGG GACCAACACT AGAATATCGC CCTCCCTCTG GTCCTGAGGG	120
AGAGGAATCC TCCGGGTTT CCAGATCCTG TACCAGAGAG TGACTCTGAG GTTCCGCCCT	180
GCTCTCTGAG CACAATTAAG GGATAAAATC TCTGAAGGAA TGACGGGAAG ACGATCCCTC	240
GAATACTGAT GAGTGGTTCC CTTTGACACA CACAGGCAGC AGCCTGGGC CCGTGACTTT	300
TCCTCTCAGG CCTTGTCTC TGCTTCACAC TCAATGTGTG TGGGGGTCTG AGTCCAGCAC	360
TTCTGAGTCC TTCAGCCTCC ACTCAGGTCA GGACCAGAAG TCGCTGTTCC CTCTTCAGGG	420
ACTAGAATTG TCCACGGAAT AGGAGATTAT CCCAGGTGCC TGTGTCCAGG CTGGTGTCTG	480
GGTTCTGTGC TCCCTTCCCCC ATCCCAGGTG TCCTGTCCAT TCTCAAGATA GCCACATGTG	540
TGCTGGAGGA GTGTCCCATG ACAGATGCAA AATGCCTGAA TGATCTGACT CTTCCCTGACA	600
G	601

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 601 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(v) ORIGINAL SOURCE:

(A) ORGANISM: human

(ix) FEATURE:

(A) NAME/KEY: HLA-A Intron 3 Allele A* 0217

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

GTACCAGGGG CCACGGGGCG CCTCCCTGAT CGCCTGAGA TCTCCGGGC TGGCCTCCCA	60
CAAGGAGGGG AGACAATTGG GACCAACACT AGAATATCGC CCTCCCTCTG GTCCTGAGGG	120
AGAGGAATCC TCCGGGTTT CCAGATCCTG TACCAGAGAG TGACTCTGAG GTTCCGCCCT	180
GCTCTCTGAG CACAATTAAG GGATAAAATC TCTGAAGGAA TGACGGGAAG ACGATCCCTC	240
GAATACTGAT GAGTGGTTCC CTTTGACACA CACAGGCAGC AGCCTGGGC CCGTGACTTT	300
TCCTCTCAGG CCTTGTCTC TGCTTCACAC TCAATGTGTG TGGGGGTCTG AGTCCAGCAC	360
TTCTGAGTCC TTCAGCCTCC ACTCAGGTCA GGACCAGAAG TCGCTGTTCC CTCTTCAGGG	420
ACTAGAATTG TCCACGGAAT AGGAGATTAT CCCAGGTGCC TGTGTCCAGG CTGGTGTCTG	480

GGTTCTGTGC TCCCTTCCCC ATCCCAGGTG TCCTGTCCAT TCTCAAGATA GCCACATGTG	540
TGCTGGAGGA GTGTCCCAGT ACAGATGCAA AATGCCTGAA TGATCTGACT CTTCCGTACA	600
G	601

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 6801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

GTACCAGGGG CCACGGGGCG CCTCCCTGAT CGCCTGTAGA TCTCCCGGGC TGGCCTCCCA	60
CAAGGAGGGG AGACAATTGG GACCAACACT AGAATATCGC CCTCCCTCTG GTCCTGAGGG	120
AGAGGAATCC TCCTGGGTTT CCAGATCCTG TACCAGAGAG TGACTCTGAG GTTCCGCCCT	180
GCTCTCTGAG CACAATTAAG GGATAAAATC TCTGAAGGAA TGACGGGAAG ACGATCCCTC	240
GAATACTGAT GAGTGGTTCC CTTTGACACA CACAGGCAGC AGCCTTGGGC CCGTGACTTT	300
TCCTCTCAGG CCTTGTTCTC TGCTTCACAC TCAATGTGTG TGGGGGTCTG AGTCCAGCAC	360
TTCTGAGTCC CTCAGCCTCC ACTCAGGTCA GGACCAGAAG TCGCTGTTCC CTCTTCAGGG	420
ACTAGAATTTC TCCACGGAAT AGGAGATTAT CCCAGGTGCC TGTGTCCAGG CTGGTGCTCG	480
GGTTCTGTGC TCCCTTCCCC ATCCCAGGTG TCCTGTCCAT TCTCAAGATA GCCACATGTG	540
TGCTGGAGGA GTGTCCCAGT ACAGATGCAA AATGCCTGAA TGATCTGACT CTTCCGTACA	600
G	601

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 6802

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

GTACCAGGGG CCACGGGGCG CCTCCCTGAT CGCCTGTAGA TCTCCCGGGC TGGCCTCCCA	60
CAAGGAGGGG AGACAATTGG GACCAACACT AGAATATCGC CCTCCCTCTG GTCCTGAGGG	120
AGAGGAATCC TCCTGGGTTT CCAGATCCTG TACCAGAGAG TGACTCTGAG GTTCCGCCCT	180
GCTCTCTGAG CACAATTAAG GGATAAAATC TCTGAAGGAA TGACGGGAAG ACGATCCCTC	240

GAATACTGAT	GAGTGGTTCC	CTTGACACA	CACAGGCAGC	AGCCTGGGC	CCGTGACTTT	3 00
TCCTCTCAGG	CCTTGTTC	TGCTTCACAC	TCAATGTGTG	TGGGGGTCTG	AGTCCAGCAC	3 60
TTCTGAGTCC	CTCAGCCTCC	ACTCAGGTCA	GGACCAGAAG	TCGCTGTTCC	CTCTTCAGGG	4 20
ACTAGAATTT	TCCACGGAAT	AGGAGATTAT	CCCAGGTGCC	TGTGTCCAGG	CTGGTGTCTG	4 80
GGTTCTGTGC	TCCCTTCCCC	ATCCCAGGTG	TCCTGTCCAT	TCTCAAGATA	GCCACATGTG	5 40
TGCTGGAGGA	GTGTCCCATG	ACAGATGCAA	AATGCCTGAA	TGATCTGACT	CTTCCTGACA	6 00
G						6 01

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 6901

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

GTACCAGGGG	CCACGGGGCG	CCTCCCTGAT	CGCCTGTAGA	TCTCCCGGGC	TGGCCTCCCA	60
CAAGGAGGGG	AGACAATTGG	GACCAACACT	AGAATATCGC	CCTCCCTCTG	GTCCTGAGGG	120
AGAGGAATCC	TCCCTGGTTT	CCAGATCCTG	TACCAGAGAG	TGACTCTGAG	GTTCCGCCCT	180
GCTCTCTGAG	CACAATTAAG	GGATAAAATC	TCTGAAGGAA	TGACGGGAAG	ACGATCCCTC	240
GAATACTGAT	GAGTGGTTCC	CTTGACACA	CACAGGCAGC	AGCCTGGGC	CCGTGACTTT	3 00
TCCTCTCAGG	CCTTGTTC	TGCTTCACAC	TCAATGTGTG	TGGGGGTCTG	AGTCCAGCAC	3 60
TTCTGAGTCC	CTCAGCCTCC	ACTCAGGTCA	GGACCAGAAG	TCGCTGTTCC	CTCTTCAGGG	4 20
ACTAGAATTT	TCCACGGAAT	AGGAGATTAT	CCCAGGTGCC	TGTGTCCAGG	CTGGTGTCTG	4 80
GGTTCTGTGC	TCCCTTCCCC	ATCCCAGGTG	TCCTGTCCAT	TCTCAAGATA	GCCACATGTG	5 40
TGCTGGAGGA	GTGTCCCATG	ACAGATGCAA	AATGCCTGAA	TGATCTGACT	CTTCCTGACA	6 00
G						6 01

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 2301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

GTACCAGGGG CCACGGGGCG CCTACCTGAT CGCCTGAGG TCTCCGGGC TGGCCTCCCA	60
CAAGGAGGGG AGACAATTGG GACCAACACT AGAATATCGC CCTCCCTCTG GTCCTGAGGG	120
AGAGGAATCC TCCTGGTTT CCAGATCCTG TACCAGAGAG TGACTCTGAG GTTCCGCCCT	180
GCTCTCTGAG CACAATTAAG GGATAAAATC TCTGACGGAA TGACGGAAAG ACGATCCCTC	240
GAATACTGAT GACTGGTTCC CTTTGACACC GGCAGCAGCC TTGGGACCGT GACTTTCCCT	300
CTCAGGCCCT GTTCTCTGCT TCACACTCAA TGTGTGTGGG GGTCTGAGTC CAGCACTTCT	360
GAGTCCCTCA GCCTCCACTC AGGTCAAGGAC CAGAAGTCGC TGTTCCCTCC TCAGGGAAATA	420
GAAGATTATC CCAGGTGCCT GTGTCCAGGC TGGTGTCTGG GTTCTGTGCT CTCTTCCCA	480
TCCCGGGTGT CCTGTCCATT CTCAAGATGG CCACATGCAT GCTGGTGGAG TGTCCCATGA	540
CAGATGCAAA ATGCCTGAAT TTTCTGACTC TTCCCGTCAG	580

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 2402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

GTACCAGGGG CCACGGGGCG CCTACCTGAT CGCCTGAGG TCTCCGGGC TGGCCTCCCA	60
CAAGGAGGGG AGACAATTGG GACCAACACT AGAATATCGC CCTCCCTCTG GTCCTGAGGG	120
AGAGGAATCC TCCTGGTTT CCAGATCCTG TACCAGAGAG TGACTCTGAG GTTCCGCCCT	180
GCTCTCTGAG CACAATTAAG GGATAAAATC TCTGACGGAA TGACGGAAAG ACGATCCCTC	240
GAATACTGAT GACTGGTTCC CTTTGACACC GGCAGCAGCC TTGGGACCGT GACTTTCCCT	300
CTCAGGCCCT GTTCTCTGCT TCACACTCAA TGTGTGTGGG GGTCTGAGTC CAGCACTTCT	360
GAGTCCCTCA GCCTCCACTC AGGTCAAGGAC CAGAAGTCGC TGTTCCCTCC TCAGGGAAATA	420
GAAGATTATC CCAGGTGCCT GTGTCCAGGC TGGTGTCTGG GTTCTGTGCT CTCTTCCCA	480
TCCCGGGTGT CCTGTCCATT CTCAAGATGG CCACATGCAT GCTGGTGGAG TGTCCCATGA	540
CAGATGCAAA ATGCCTGAAT TTTCTGACTC TTCCCGTCAG	580

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 2403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

GTACCAGGGG	CCACGGGGCG	CCTACCTGAT	CGCCTGTAGG	TCTCCCGGGC	TGGCCTCCCA	60
CAAGGAGGGG	AGACAATTGG	GACCAACACT	AGAATATCGC	CCTCCCTCTG	GTCCTGAGGG	120
AGAGGAATCC	TCCTGGGTTT	CCAGATCCTG	TACCAGAGAG	TGACTCTGAG	GTTCCGCCCT	180
GCTCTCTGAG	CACAATTAAG	GGATAAAATC	TCTGACGGAA	TGACGGAAAG	ACGATCCCTC	240
GAATACTGAT	GACTGGTTCC	CTTTGACACC	GGCAGCAGCC	TTGGGACCGT	GACTTTCCCT	300
CTCAGGCCCT	GTTCTCTGCT	TCACACTCAA	TGTGTGTGGG	GGTCTGAGTC	CAGCACTTCT	360
GAGTCCCTCA	GCCTCCACTC	AGGTCAAGGAC	CAGAAGTCGC	TGTTCCCTCC	TCAGGGAATA	420
GAAGATTATC	CCAGGTGCCT	GTGTCCAGGC	TGGTGTCTGG	GTTCTGTGCT	CTCTTCCCCA	480
TCCCAGGTGT	CCTGTCCATT	CTCAAGATGG	CCACATGCAT	GCTGGTGGAG	TGTCCCATGGA	540
CAGATGCAAA	ATGCCTGAAT	TTTCTGACTC	TTCCCGTCAG			580

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 2404

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

GTACCAGGGG	CCACGGGGCG	CCTACCTGAT	CGCCTGTAGG	TCTCCCGGGC	TGGCCTCCCA	60
CAAGGAGGGG	AGACAATTGG	GACCAACACT	AGAATATCGC	CCTCCCTCTG	GTCCTGAGGG	120
AGAGGAATCC	TCCTGGGTTT	CCAGATCCTG	TACCAGAGAG	TGACTCTGAG	GTTCCGCCCT	180
GCTCTCTGAG	CACAATTAAG	GGATAAAATC	TCTGACGGAA	TGACGGAAAG	ACGATCCCTC	240
GAATACTGAT	GACTGGTTCC	CTTTGACACC	GGCAGCAGCC	TTGGGACCGT	GACTTTCCCT	300
CTCAGGCCCT	GTTCTCTGCT	TCACACTCAA	TGTGTGTGGG	GGTCTGAGTC	CAGCACTTCT	360
GAGTCCCTCA	GCCTCCACTC	AGGTCAAGGAC	CAGAAGTCGC	TGTTCCCTCC	TCAGGGAATA	420
GAAGATTATC	CCAGGTGCCT	GTGTCCAGGC	TGGTGTCTGG	GTTCTGTGCT	CTCTTCCCCA	480
TCCCAGGTGT	CCTGTCCATT	CTCAAGATGG	CCACATGCAT	GCTGGTGGAG	TGTCCCATGGA	540
CAGATGCAAA	ATGCCTGAAT	TTTCTGACTC	TTCCCGTCAG			579

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 2407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

GTACCAGGGG	CCACGGGGCG	CCTACCTGAT	CGCCTGTAGG	TCTCCCGGGC	TGGCCTCCCA	60
CAAGGAGGGG	AGACAATTGG	GACCAACACT	AGAATATCGC	CCTCCCTCTG	GTCCTGAGGG	120
AGAGGAATCC	TCCTGGGTTT	CCAGATCCTG	TACCAGAGAG	TGACTCTGAG	GTTCCGCCCT	180
GCTCTCTGAG	CACAATTAAG	GGATAAAATC	TCTGACGGAA	TGACGGAAAG	ACGATCCCTC	240
GAATACTGAT	GACTGGTTCC	CTTTGACACC	GGCAGCAGCC	TTGGGACCGT	GACTTTCCCT	300
CTCAGGCCCT	GTTCTCTGCT	TCACACTCAA	TGTGTGTGGG	GGTCTGAGTC	CAGCACTTCT	360
GAGTCCCTCA	GCCTCCACTC	AGGTCAGGAC	CAGAAGTCGC	TGTTCCCTCC	TCAGGGAAATA	420
GAAGATTATC	CCAGGTGCCT	GTGTCCAGGC	TGGTGTCTGG	GTTCTGTGCT	CTCTTCCCCA	480
TCCCAGGTGT	CCTGTCCATT	CTCAAGATGG	CCACATGCAT	GCTGGTGGAG	TGTCCCATGGA	540
CAGATGCAAA	ATGCCTGAAT	TTTCTGACTC	TTCCCGTCAG			580

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 2407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

GTACCAGGGG	CCACGGGGCG	CCTACCTGAT	CGCCTGTAGG	TCTCCCGGGC	TGGCCTCCCA	60
CAAGGAGGGG	AGACAATTGG	GACCAACACT	AGAATATCGC	CCTCCCTCTG	GTCCTGAGGG	120
AGAGGAATCC	TCCTGGGTTT	CCAGATCCTG	TACCAGAGAG	TGACTCTGAG	GTTCCGCCCT	180
GCTCTCTGAG	CACAATTAAG	GGATAAAATC	TCTGACGGAA	TGACGGAAAG	ACGATCCCTC	240
GAATACTGAT	GACTGGTTCC	CTTTGACACC	GGCAGCAGCC	TTGGGACCGT	GACTTTCCCT	300
CTCAGGCCCT	GTTCTCTGCT	TCACACTCAA	TGTGTGTGGG	GGTCTGAGTC	CAGCACTTCT	360
GAGTCCCTCA	GCCTCCACTC	AGGTCAGGAC	CAGAAGTCGC	TGTTCCCTCC	TCAGGGAAATA	420
GAAGATTATC	CCAGGTGCCT	GTGTCCAGGC	TGGTGTCTGG	GTTCTGTGCT	CTCTTCCCCA	480
TCCCAGGTGT	CCTGTCCATT	CTCAAGATGG	CCACATGCAT	GCTGGTGGAG	TGTCCCATGGA	540
CAGATGCAAA	ATGCCTGAAT	TTTCTGACTC	TTCCCGTCAG			580

(2) INFORMATION FOR SEQ ID NO:164:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:

(A) NAME/KEY: HLA-A Intron 3 Allele A* 2501

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

GTACCAGGGG	CCACGGGGCG	CCTCCCTGAT	CGCCTGTAGA	TCTCCCGGGC	TGGCCTCCCA	60
CAAGGAGGGG	AGACAATTGG	GACCAACACT	AGAATATCGC	CCTCCCTCTG	GTCCTGAGGG	120
AGAGGAATCC	TCCTGGGTTT	CCAGATCCTG	TACCAGAGAG	TGACTCTGAG	GTTCCGCCCT	180
GCTCTCTGAG	CACAATTAAG	GGATAAAATC	TCTGAAGGAA	TGACGGGAAG	ACGATCCCTC	240
GAATACTGAT	GAGTGGTTCC	CTTGACACA	CACCGGCAGC	AGCCTTGGGC	CCGTGACTTT	300
TCCTCTCAGG	CCTTGTCTC	TGCTTCACAC	TCAATGTGTG	TGGGGGTCTG	AGTCCAGCAC	360
TTCTGAGTCC	CTCAGCCTCC	ACTCAGGTCA	GGACCAGAAG	TCGCTGTTCC	CTCTTCAGGG	420
ACTAGAATTT	TCCACGGAAT	AGGAGATTAT	CCCAGGTGCC	TGTGTCCAGG	CTGGTGTCTG	480
GGTTCTGTGC	TCCCTTCCCC	ATCCCAGGTG	TCCTGTCCAT	TCTCAAGATA	GCCACATGTG	540
TGCTGGAGGA	GTGTCCCAGT	ACAGATGCAA	AATGCCTGAA	TGTTCTGACT	CTTCCTGACA	600
G						601

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 2601

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

GTACCAGGGG	CCACGGGGCG	CCTCCCTGAT	CGCCTGTAGA	TCTCCCGGGC	TGGCCTCCCA	60
CAAGGAGGGG	AGACAATTGG	GACCAACACT	AGAATATCGC	CCTCCCTCTG	GTCCTGAGGG	120
AGAGGAATCC	TCCTGGGTTT	CCAGATCCTG	TACCAGAGAG	TGACTCTGAG	GTTCCGCCCT	180
GCTCTCTGAG	CACAATTAAG	GGATAAAATC	TCTGAAGGAA	TGACGGGAAG	ACGATCCCTC	240
GAATACTGAT	GAGTGGTTCC	CTTGACACA	CACCGGCAGC	AGCCTTGGGC	CCGTGACTTT	300
TCCTCTCAGG	CCTTGTCTC	TGCTTCACAC	TCAATGTGTG	TGGGGGTCTG	AGTCCAGCAC	360
TTCTGAGTCC	CTCAGCCTCC	ACTCAGGTCA	GGACCAGAAG	TCGCTGTTCC	CTCTTCAGGG	420
ACTAGAATTT	TCCACGGAAT	AGGAGATTAT	CCCAGGTGCC	TGTGTCCAGG	CTGGTGTCTG	480
GGTTCTGTGC	TCCCTTCCCC	ATCCCAGGTG	TCCTGTCCAT	TCTCAAGATA	GCCACATGTG	540
TGCTGGAGGA	GTGTCCCAGT	ACAGATGCAA	AATGCCTGAA	TGTTCTGACT	CTTCCTGACA	600
G						601

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no

- (iv) ANTI-SENSE: no
- (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 3402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

GTACCAGGGG CCACGGGGCG CCTCCCTGAT CGCCTGTAGA TCTCCGGGC TGGCCTCCCA	60
CAAGGAGGGG AGACAATTGG GACCAACACT AGAATATCGC CCTCCCTCTG GTCCTGAGGG	120
AGAGGAATCC TCCTGGGTTT CCAGATCCTG TACCAGAGAG TGACTCTGAG GTTCCGCCCT	180
GCTCTCTGAG CACAATTAAG GGATAAAATC TCTGAAGGAA TGACGGGAAG ACGATCCCTC	240
GAATACTGAT GAGTGGTTCC CTTTGACACA CACCGGCAGC AGCCTGGGC CCGTGACTTT	300
TCCTCTCAGG CCTTGTTCAC TGCTTCACAC TCAATGTGTG TGGGGGTCTG AGTCCAGCAC	360
TTCTGAGTCC CTCAGCCTCC ACTCAGGTCA GGACCAGAAG TCGCTGTTCC CTCTTCAGGG	420
ACTAGAATTT TCCACGGAAT AGGAGATTAT CCCAGGTGCC TGTGTCCAGG CTGGTGTCTG	480
GGTTCTGTGC TCCCTTCCCCC ATCCCAGGTG TCCGTCCAT TCTCAAGATA GCCACATGTG	540
TGCTGGAGGA GTGTCCCATG ACAGATGCAA AATGCCTGAA TGTCTGACT CTTCCTGACA	600
G	601

(2) INFORMATION FOR SEQ ID NO:167:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 601 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 4301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

GTACCAGGGG CCACGGGGCG CCTCCCTGAT CGCCTGTAGA TCTCCGGGC TGGCCTCCCA	60
CAAGGAGGGG AGACAATTGG GACCAACACT AGAATATCGC CCTCCCTCTG GTCCTGAGGG	120
AGAGGAATCC TCCTGGGTTT CCAGATCCTG TACCAGAGAG TGACTCTGAG GTTCCGCCCT	180
GCTCTCTGAG CACAATTAAG GGATAAAATC TCTGAAGGAA TGACGGGAAG ACGATCCCTC	240
GAATACTGAT GAGTGGTTCC CTTTGACACA CACCGGCAGC AGCCTGGGC CCGTGACTTT	300
TCCTCTCAGG CCTTGTTCAC TGCTTCACAC TCAATGTGTG TGGGGGTCTG AGTCCAGCAC	360
TTCTGAGTCC CTCAGCCTCC ACTCAGGTCA GGACCAGAAG TCGCTGTTCC CTCTTCAGGG	420
ACTAGAATTT TCCACGGAAT AGGAGATTAT CCCAGGTGCC TGTGTCCAGG CTGGTGTCTG	480
GGTTCTGTGC TCCCTTCCCCC ATCCCAGGTG TCCGTCCAT TCTCAAGATA GCCACATGTG	540
TGCTGGAGGA GTGTCCCATG ACAGATGCAA AATGCCTGAA TGTCTGACT CTTCCTGACA	600
G	601

(2) INFORMATION FOR SEQ ID NO:168:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 601 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 6601

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

GTACCAGGGG CCACGGGGCG CCTCCCTGAT CGCCTGTAGA TCTCCGGGC TGGCCTCCCA	60
CAAGGAGGGG AGACAATTGG GACCAACACT AGAATATCGC CCTCCCTCTG GTCCTGAGGG	120
AGAGGAATCC TCCTGGTTT CCAGATCCTG TACCAGAGAG TGACTCTGAG GTTCCGCCCT	180
GCTCTCTGAG CACAATTAAG GGATAAAATC TCTGAAGGAA TGACGGGAAG ACGATCCCTC	240
GAATACTGAT GAGTGGTTCC CTTTGACACA CACCGGCAGC AGCCTGGGC CCGTGACTTT	300
TCCTCTCAGG CCTTGGTTCTC TGCTTCACAC TCAATGTGTG TGGGGGTCTG AGTCCAGCAC	360
TTCTGAGTCC CTCAGCCTCC ACTCAGGTCA GGACCAGAAAG TCGCTGTTCC CTCTTCAGGG	420
ACTAGAATTTC TCCACGGAAT AGGAGATTAT CCCAGGTGCC TGTGTCCAGG CTGGTGTCTG	480
GGTTCTGTGC TCCCTTCCCCC ATCCCAGGTG TCCTGTCCAT TCTCAAGATA GCCACATGTG	540
TGCTGGAGGA GTGTCCCAGT ACAGATGCAA AATGCCTGAA TGTTCTGACT CTTCCGTGACA	600
G	601

(2) INFORMATION FOR SEQ ID NO:169:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 601 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 6602

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

GTACCAGGGG CCACGGGGCG CCTCCCTGAT CGCCTGTAGA TCTCCGGGC TGGCCTCCCA	60
CAAGGAGGGG AGACAATTGG GACCAACACT AGAATATCGC CCTCCCTCTG GTCCTGAGGG	120
AGAGGAATCC TCCTGGTTT CCAGATCCTG TACCAGAGAG TGACTCTGAG GTTCCGCCCT	180
GCTCTCTGAG CACAATTAAG GGATAAAATC TCTGAAGGAA TGACGGGAAG ACGATCCCTC	240
GAATACTGAT GAGTGGTTCC CTTTGACACA CACCGGCAGC AGCCTGGGC CCGTGACTTT	300
TCCTCTCAGG CCTTGGTTCTC TGCTTCACAC TCAATGTGTG TGGGGGTCTG AGTCCAGCAC	360
TTCTGAGTCC CTCAGCCTCC ACTCAGGTCA GGACCAGAAAG TCGCTGTTCC CTCTTCAGGG	420
ACTAGAATTTC TCCACGGAAT AGGAGATTAT CCCAGGTGCC TGTGTCCAGG CTGGTGTCTG	480
GGTTCTGTGC TCCCTTCCCCC ATCCCAGGTG TCCTGTCCAT TCTCAAGATA GCCACATGTG	540
TGCTGGAGGA GTGTCCCAGT ACAGATGCAA AATGCCTGAA TGTTCTGACT CTTCCGTGACA	600
G	601

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 6603

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

GTACCAGGGG CCACGGGGCG CCTCCCTGAT CGCCTGTAGA TCTCCCGGGC TGGCCTCCCA	60
CAAGGAGGGG AGACAATTGG GACCAACACT AGAATATCGC CCTCCCTCTG GTCCTGAGGG	120
AGAGGAATCC TCCTGGGTTT CCAGATCCTG TACCAGAGAG TGACTCTGAG GTTCCGCCCT	180
GCTCTCTGAG CACAATTAAG GGATAAAATC TCTGAAGGAA TGACGGGAAG ACGATCCCTC	240
GAATACTGAT GAGTGGTTCC CTTTGACACA CACCGGCAGC AGCCTGGGC CCGTGACTTT	300
TTCTCTCAGG CCTTGTTCTC TGCTTCACAC TCAATGTGTG TGGGGGTCTG AGTCCAGCAC	360
TTCTGAGTCC CTCAGCCTCC ACTCAGGTCA GGACCAGAAG TCGCTGTTCC CTCTTCAGGG	420
ACTAGAATTT TCCACGGAAT AGGAGATTAT CCCAGGTGCC TGTGTCCAGG CTGGTGTCTG	480
GGTTCTGTGC TCCCTTCCCC ATCCCAGGTG TCCTGTCCAT TCTCAAGATA GCCACATGTG	540
TGCTGGAGGA GTGTCCCAGT ACAGATGCAA AATGCCTGAA TGTCTGACT CTTCCCTGACA	600
G	601

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 2901

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

GTACCGGGGG CCACGGGGCG CCTCCCTGAT CGCCTGTAGA TCTCCCGGGC TGGCCTCCCA	60
CAAGGAGGGG AGACAATTGG GACCAACACT AGAATATCGC CCTCCCTCTG GTCCTGAGGG	120
AGAGGAATCC TCCTGGGTTT CCAGATCCTG TACCAGAGAG TGACTCTGAG GTTCCGCCCT	180
GCTCTCTGAG CACAATTAAG GGATAAAATC TCTGAAGGAA TGACGGGAAG ACGATCCCTC	240
GAATACTGAT GAGTGGTTCC CTTTGACACA CACCGGCAGC AGCCTGGGC CCGTGACTTT	300
TCCTCTCAGG CCTTGTTCTC TGCTTCACAC TCAATGTGTG TGGGGGTCTG AGTCCAGCAC	360
TTCTGAGTCC CTCAGCCTCC ACTCAGGTCA GGACCAGAAG TCGCTGTTCC CTCTTCAGGG	420
ACTAGAATTT TCCACGGAAT AGGAGATTAT CCCAGGTGCC TGTGTCCAGG CTGGTGTCTG	480
GGTTCTGTGC TCCCTTCCCC ATCCCAGGTG TCCTGTCCAT TCTCAAGATA GCCACATGTG	540
TGCTGGAGGA GTGTCCCAGT ACAGATGCAA AATGCCTGAA TGTCTGACT CTTCCCTGACA	600

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 2902

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

GTACCGGGGG CCACGGGGCG CCTCCCTGAT CGCCTGAGA TCTCCGGGC TGGCCTCCCA	60
CAAGGAGGGG AGACAATTGG GACCAACACT AGAATATCGC CCTCCCTCTG GTCCTGAGGG	120
AGAGGAATCC TCTGGGTTT CCAGATCCTG TACCAGAGAG TGACTCTGAG GTTCCGCCCT	180
GCTCTGTGAG CACAATTAAG GGATAAAATC TCTGAAGGAA TGACGGGAAG ACGATCCCTC	240
GAATACTGAT GAGTGGTTCC CTTTGACACA CACCGGCAGC AGCCTTGGGC CCGTGACTTT	300
TCCTCTCAGG CCTTGTTCTC TGCTTCACAC TCAATGTGTG TGGGGGTCTG AGTCCAGCAC	360
TTCTGAGTCC CTCAGCCTCC ACTCAGGTCA GGACCAGAAG TCGCTGTTCC CTCTTCAGGG	420
ACTAGAATTG TCCACGGAAT AGGAGATTAT CCCAGGTGCC TGTGTCCAGG CTGGTGCTG	480
GGTTCTGTGC TCCCTTCCCC ATCCCAGGTG TCCTGTCCAT TCTCAAGATA GCCACATGTG	540
TGCTGGAGGA GTGTCCCAGT ACAGATGCAA AATGCCTGAA TGTTCTGACT CTTCCCTGACA	600
G	601

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 3101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

GTACCAAGGGG CCACGGGGCG CCTCCCTGAT CGCCTGAGA TCTCCGGGC TGGCCTCCCA	60
CAAGGAGGGG AGACAATTGG GACCAACACT AGAATATCAC CCTCCCTCTG GTCCTGAGGG	120
AGAGGAATCC TCTGGGTTT CCAGATCCTG TACCAGAGAG TGACTCTGAG GTTCCGCCCT	180
GCTCTGTGAG CACAATTAAG GGATAAAATC TCTGAAGGAA TGACGGGAAG ACGATCCCTC	240
GAATACTGAT GAGTGGTTCC CTTTGACACA CACCGGCAGC AGCCTTGGGC CCGTGACTTT	300
TCCTCTCAGG CCTTGTTCTC TGCTTCACAC TCAATGTGTG TGGGGGTCTG AGTCCAGCAC	360

TTCTGAGTCC CTCAGCCTCC ACTCAGGTCA GGACCAGAAG TCGCTGTTCC CTCTTCAGGG	420
ACTAGAAATT TCCACGGAAT AGGAGATTAT CCCAGGTGCC TGTGTCCAGG CTGGTGTCTG	480
GGTTCTGTGC TCCCTTCCCC ATCCCAGGTG TCCTGTCCAT TCTCAAGATA GCCACATGTG	540
TGCTGGAGGA GTGTCCCATT ACAGATGCAA AATGCCTGAA TGTTCTGACT CTTCCGTACA	600
G	601

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 3201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

GTACCAGGGG CCACGGGGCG CCTCCCTGAT CGCCTGAGA TCTCCCGGGC TGGCCTCCCA	60
CAAGGAGGGG AGACAATTGG GACCAACACT AGAATATCGC CCTCCCTCTG GTCCTGAGGG	120
AGAGGAATCC TCCTGGGTTT CCAGATCCTG TACCAGAGAG TGACTCTGAG GTTCCGCCCT	180
GCTCTCTGAG CACAATTAAG GGATAAAATC TCTGAAGGAA TGACCGGAAG ACGATCCCTC	240
GAATACTGAT GAGTGGTTCC CTTTGACACA CACCGGCAGC AGCCTTGGGC CCGTGACTTT	300
TCCTCTCAGG CCTGTGTTCTC TGCTTCACAC TCAATGTGTG TGGGGGTCTG AGTCCAGCAC	360
TTCTGAGTCC CTCAGCCTCC ACTCAGGTCA GGACCAGAAG TCGCTGTTCC CTCTTCAGGG	420
ACTAGAAATT TCCACGGAAT AGGAGATTAT CCCAGGTGCC TGTGTCCAGG CTGGTGTCTG	480
GGTTCTGTGC TCCCTTCCCC ATCCCAGGTG TCCTGTCCAT TCTCAAGATA GCCACATGTG	540
TGCTGGAGGA GTGTCCCATT ACAGATGCAA AATGCCTGAA TGTTCTGACT CTTCCGTACA	600
G	601

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 3301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

GTACCAGGGG CCACGGGGCG CCTCCCTGAT CGCCTGAGA TCTCCCGGGC TGGCCTCCCA	60
CAAGGAGGGG AGACAATTGG GACCAACACT AGAATATCAC CCTCCCTCTG GTCCTGAGGG	120

AGAGGAATCC	TCCTGGTTT	CCAGATCCTG	TACCAGAGAG	TGACTCTGAG	GTTCCGCCCT	180
GCTCTGTGAG	CACAATTAAAG	GGATAAAATC	TCTGAAGGAA	TGACGGGAAG	ACGATCCCTC	240
GAATACTGAT	GAGTGGTCC	CTTGACACA	CACCGGCAGC	AGCCTTGGGC	CCGTGACTTT	300
TCCTCTCAGG	CCTTGTCTC	TGCTTCACAC	TCAATGTGTG	TGGGGTCTG	AGTCCAGCAC	360
TTCTGAGTCC	CTCAGCCTCC	ACTCAGGTCA	GGACCAGAAG	TCGCTGTTCC	CTCTTCAGGG	420
ACTAGAAATT	TCCACGGAAT	AGGAGATTAT	CCCAGGTGCC	TGTGTCCAGG	CTGGTGTCTG	480
GGTTCTGTGC	TCCCTTCCCC	ATCCCAGGTG	TCCTGTCCAT	TCTCAAGATA	GCCACATGTG	540
TGCTGGAGGA	GTGTCCCATT	ACAGATGCAA	AATGCCTGAA	TGTTCTGACT	CTTCCTGACA	600
G						601

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 3303

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

GTACCAGGGG	CCACGGGGCG	CCTCCCTGAT	CGCCTGTAGA	TCTCCCGGGC	TGGCCTCCCA	60
CAAGGAGGGG	AGACAATTGG	GACCAACACT	AGAATATCAC	CCTCCCTCTG	GTCCTGAGGG	120
AGAGGAATCC	TCCTGGTTT	CCAGATCCTG	TACCAGAGAG	TGACTCTGAG	GTTCCGCCCT	180
GCTCTGTGAG	CACAATTAAAG	GGATAAAATC	TCTGAAGGAA	TGACGGGAAG	ACGATCCCTC	240
GAATACTGAT	GAGTGGTCC	CTTGACACA	CACCGGCAGC	AGCCTTGGGC	CCGTGACTTT	300
TCCTCTCAGG	CCTTGTCTC	TGCTTCACAC	TCAATGTGTG	TGGGGTCTG	AGTCCAGCAC	360
TTCTGAGTCC	CTCAGCCTCC	ACTCAGGTCA	GGACCAGAAG	TCGCTGTTCC	CTCTTCAGGG	420
ACTAGAAATT	TCCACGGAAT	AGGAGATTAT	CCCAGGTGCC	TGTGTCCAGG	CTGGTGTCTG	480
GGTTCTGTGC	TCCCTTCCCC	ATCCCAGGTG	TCCTGTCCAT	TCTCAAGATA	GCCACATGTG	540
TGCTGGAGGA	GTGTCCCATT	ACAGATGCAA	AATGCCTGAA	TGTTCTGACT	CTTCCTGACA	600
G						601

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 7401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

GTACCAGGGG CCACGGGGCG CCTCCCTGAT CGCCTGAGA TCTCCGGGC TGGCCTCCCA	60
CAAGGAGGGG AGACAATTGG GACCAACACT AGAATATCGC CCTCCCTCTG GTCCTGAGGG	120
AGAGGAATCC TCCTGGGTTT CCAGATCCTG TACCAGAGAG TGACTCTGAG GTTCCGCCCT	180
GCTCTCTGAG CACAATTAAG GGATAAAATC TCTGAAGGAA TGACGGGAAG ACGATCCCTC	240
GAATACTGAT GAGTGGTTCC CTTTGACACA CACCGGCAGC AGCCTTGGGC CCGTGACTTT	300
TCCTCTCAGG CCTTGTTCCTC TGCTTCACAC TCAATGTGTG TGGGGGTCTG AGTCCAGCAC	360
TTCTGAGTCC CTCAGCCTCC ACTCAGGTCA GGACCAGAAG TCGCTGTTCC CTCTTCAGGG	420
ACTAGAATT TTCCACGGAAT AGGAGATTAT CCCAGGTGCC TGTGTCCAGG CTGGTGTCTG	480
GGTTCTGTGC TCCCTTCCCC ATCCCAGGTG TCCTGTCCAT TCTCAAGATA GCCACATGTG	540
TGCTGGAGGA GTGTCCCATG ACAGATGCAA AATGCCTGAA TGTTCTGACT CTTCCTGACA	600
G	601

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: genomic DNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 7402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

GTACCAGGGG CCACGGGGCG CCTCCCTGAT CGCCTGAGA TCTCCGGGC TGGCCTCCCA	60
CAAGGAGGGG AGACAATTGG GACCAACACT AGAATATCGC CCTCCCTCTG GTCCTGAGGG	120
AGAGGAATCC TCCTGGGTTT CCAGATCCTG TACCAGAGAG TGACTCTGAG GTTCCGCCCT	180
GCTCTCTGAG CACAATTAAG GGATAAAATC TCTGAAGGAA TGACGGGAAG ACGATCCCTC	240
GAATACTGAT GAGTGGTTCC CTTTGACACA CACCGGCAGC AGCCTTGGGC CCGTGACTTT	300
TCCTCTCAGG CCTTGTTCCTC TGCTTCACAC TCAATGTGTG TGGGGGTCTG AGTCCAGCAC	360
TTCTGAGTCC CTCAGCCTCC ACTCAGGTCA GGACCAGAAG TCGCTGTTCC CTCTTCAGGG	420
ACTAGAATT TTCCACGGAAT AGGAGATTAT CCCAGGTGCT TGTGTCCAGG CTGGTGTCTG	480
GGTTCTGTGC TCCCTTCCCC ATCCCAGGTG TCCTGTCCAT TCTCAAGATA GCCACATGTG	540
TGCTGGAGGA GTGTCCCATG ACAGATGCAA AATGCCTGAA TGTTCTGACT CTTCCTGACA	600
G	601

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: genomic DNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human

120

(ix) FEATURE:

(A) NAME/KEY: HLA-A Intron 3 Allele A* 7403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

GTACCAGGGG CCACGGGGCG CCTCCCTGAT CGCCTGTAGA TCTCCGGGC TGGCCTCCCA	60
CAAGGAGGGG AGACAATTGG GACCAACACT AGAATATCGC CCTCCCTCTG GTCCTGAGGG	120
AGAGGAATCC TCCTGGTTT CCAGATCCTG TACCAGAGAG TGACTCTGAG GTTCCGCCCT	180
GCTCTCTGAG CACAATTAAG GGATAAAAATC TCTGAAGGAA TGACGGGAAG ACGATCCCTC	240
GAATACTGAT GAGTGGTTCC CTTTGACACA CACCGGCAGC AGCCTGGGC CCGTGACTTT	300
TCCTCTCAGG CCTTGTTC TGCTTCACAC TCAATGTGTG TGGGGGTCTG AGTCCAGCAC	360
TTCTGAGTCC CTCAGCCTCC ACTCAGGTCA GGACCAGAAG TCGCTGTTCC CTCTTCAGGG	420
TCTAGAATTTC TCCACGGAAT AGGAGATTAT CCCAGGTGCC TGTGTCCAGG CTGGTGCTCG	480
GGTTCTGTGC TCCCTTCCCC ATCCCAGGTG TCCTGTCCAT TCTCAAGATA GCCACATGTG	540
TGCTGGAGGA GTGTCCCATG ACAGATGCAA AATGCCTGAA TGTTCTGACT CTTCCCTGACA	600
G	601

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 584 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 8001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

GTACCAGGGG CCACGGGGCG CCTTCCTGAT CGCCTGTAGA TCTCCGGGC TGGCCTCCCA	60
CAAGGAGGGG AGACAATTGG GACCAACACT AGATATCACC CTCCCTCTGC TCCTGAGGG	120
GAGGAATCCT CCTGGGTTTC CAGATTCTGT ACCAGAGAGT GACTCTGAGG TTCCGCCCTG	180
CTCTCTGAGC ACAATTAAGG GATAAAAATC TCTGAAGGAA TGACGGGAAG ACGATCCCTC	240
GAATACTGAT GAGTGGTTCC CTTTGACACA CACCGGCAGC AGCCTGGGC CCGTGACTTT	300
TCCTCTCAGG CCTTGTTC TGCTTCACAC TCAATATGTG TGGGGGTCTG AGTCCAGCAC	360
TTCTGAGTCT CTCAGCCTCC ACTCAGGTCA GGACCAGAAG TCGCTGTTCC CTCTTCAGGG	420
AATAGAAGAT TATCCCAGGT GCCTGTGTCC AGGCTGGTGT CTGGGTTCTG TGCTCTTTC	480
CCCATCCCAG GTGTCTGTG CATCCTCAAA ATGCCACAT GCGTGCTGGT GGAGTGTCCC	540
ATGACAGATG CAAAATGGCT GAATTTCCTG ACTCTTCCCC TCAG	584

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no

121

- (iv) ANTI-SENSE: no
- (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: IL-230m

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

GGCAGGTCTC AGCGACTG

18

(2) INFORMATION FOR SEQ ID NO:182:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: IL-226

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

CTCTGTGGGG AGAACAAAC

19

(2) INFORMATION FOR SEQ ID NO:183:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: IL-221m11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

GGGAGCGGCG CCGGGAC

17

(2) INFORMATION FOR SEQ ID NO:184:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid

122

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: IL-209

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

GAAGCAAGGG GCCCGCCC

18

(2) INFORMATION FOR SEQ ID NO:185:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: IL-214m

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

CGCCTGGCGG GGGGGCAA

18

(2) INFORMATION FOR SEQ ID NO:186:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: IL-223d

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

GTGAGTGCAG GGTCTGTGG

18

(2) INFORMATION FOR SEQ ID NO:187:

123

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: IL-225m

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

GCCGGGAGGA GGGACGGT

18

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: IL-237m14

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

GGCGCGCCCCG GCGGGGA

17

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: IL-240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

124

GGAGGGAGGGT CGGGCGGA

18

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: 5FL-243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

AGTGTCTTCG CGGTCGCTC

19

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: 5FR-257

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

CTCAGATTCT CCCCCAGACG

19

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: 5FR-273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

CATGCCGAGG GTTTCTCCCA

20

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: BP202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

CTGGCCCTGA CCCAGACCA

19

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: BP203

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

CCTGACCCAG ACCTGGGCA

19

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:

126

(A) ORGANISM: human
(ix) FEATURE:
(A) NAME/KEY: BP142

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

CAGGTATCTG CGGAGCCCC

19

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: genomic DNA
(iii) HYPOTHETICAL: no
(iv) ANTI-SENSE: no
(v) ORIGINAL SOURCE:
(A) ORGANISM: human
(ix) FEATURE:
(A) NAME/KEY: I3-236

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

GTCTGTCAGG AAGAGTCAGA A

21

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: genomic DNA
(iii) HYPOTHETICAL: no
(iv) ANTI-SENSE: no
(v) ORIGINAL SOURCE:
(A) ORGANISM: human
(ix) FEATURE:
(A) NAME/KEY: I3-239

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

GTGGAAAATT CTAGTCCCTG AA

22

(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

127

(ii) MOLECULE TYPE: genomic DNA
 (iii) HYPOTHETICAL: no
 (iv) ANTI-SENSE: no
 (v) ORIGINAL SOURCE:
 (A) ORGANISM: human
 (ix) FEATURE:
 (A) NAME/KEY: I3-246

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

AGATCTACAG GCGATCAGGA

20

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (iii) HYPOTHETICAL: no
 (iv) ANTI-SENSE: no
 (v) ORIGINAL SOURCE:
 (A) ORGANISM: human
 (ix) FEATURE:
 (A) NAME/KEY: I3-247m6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

GCCAGCCCCGG GAGTTCTAT

19

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (iii) HYPOTHETICAL: no
 (iv) ANTI-SENSE: no
 (v) ORIGINAL SOURCE:
 (A) ORGANISM: human
 (ix) FEATURE:
 (A) NAME/KEY: I3-249

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

CAGAGTCACT CTCTGGTACA G

21

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:

128

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: I3-280m18

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

GCGATCGTCT TCCCGTCAC

19

(2) INFORMATION FOR SEQ ID NO:202:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: I3-282

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

AGAGTCACTC TCTGGTACAG A

21

(2) INFORMATION FOR SEQ ID NO:203:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: 85

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

CTCCTCGTCC CCAGGCTCT

19

129

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: 118

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

TCCATGAGGT ATTTCTACAC C

21

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: 120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

GGCCAGGTTC TCAGACCA

18

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: 123

130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

CCCGGGCCCGG CAGTGGA

17

(2) INFORMATION FOR SEQ ID NO:207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: 127

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

GTTCTCACAC CATCCAGATG

20

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: 129

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

TCACACCCCTC CAGATGATGT T

21

(2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human

131

(ix) FEATURE:
(A) NAME/KEY: 134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

GGGTACCAAGC AGGACGCT

18

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: genomic DNA
(iii) HYPOTHETICAL: no
(iv) ANTI-SENSE: no
(v) ORIGINAL SOURCE:
(A) ORGANISM: human
(ix) FEATURE:
(A) NAME/KEY: 137

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

TCCATGAGGT ATTTCACCA A

21

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: genomic DNA
(iii) HYPOTHETICAL: no
(iv) ANTI-SENSE: no
(v) ORIGINAL SOURCE:
(A) ORGANISM: human
(ix) FEATURE:
(A) NAME/KEY: 140

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

GGTTCTCACA CCATCCAGAT A

21

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: genomic DNA

132

- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: 160

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

GTTCTCACAC CATCCAGAGG

20

(2) INFORMATION FOR SEQ ID NO:213:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: 167

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

GAGCCCCGCT TCAACGCC

18

(2) INFORMATION FOR SEQ ID NO:214:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: 175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

CTTCCTCCGC GGGTATGAA

19

(2) INFORMATION FOR SEQ ID NO:215:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs

133

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: 193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

GCCGGAGTAT TGGGACCG

18

(2) INFORMATION FOR SEQ ID NO:216:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: 202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

CTGGCCCTGA CCCTGACCA

19

(2) INFORMATION FOR SEQ ID NO:217:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: 98

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

GCAGGGTCCC CAGGTCCA

18

134

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: 115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

CCTCCAGGTA GGCTCTCAA

19

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: 116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

CCTCCAGGTA GGCTCTCCA

19

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: 117

135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

CCTCCAGGTA GGCTCTCTG

19

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: 126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

CCACTCCACG CACGTGCCA

19

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: 133

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

GGAGCGCGAT CCGCAGGC

18

(2) INFORMATION FOR SEQ ID NO:223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human

136

(ix) FEATURE:
(A) NAME/KEY: 135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

GGAGCCACTC CACGGACCG

19

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: genomic DNA
(iii) HYPOTHETICAL: no
(iv) ANTI-SENSE: no
(v) ORIGINAL SOURCE:
(A) ORGANISM: human
(ix) FEATURE:
(A) NAME/KEY: 136

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

GAGCCACTCC ACGCACTC

18

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: genomic DNA
(iii) HYPOTHETICAL: no
(iv) ANTI-SENSE: no
(v) ORIGINAL SOURCE:
(A) ORGANISM: human
(ix) FEATURE:
(A) NAME/KEY: 138

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

GGCCTTCACA TTCCGTGTGT T

21

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: genomic DNA

137

(iii) HYPOTHETICAL: no
(iv) ANTI-SENSE: no
(v) ORIGINAL SOURCE:
(A) ORGANISM: human
(ix) FEATURE:
(A) NAME/KEY: 142

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

CAGGTATCTG CGGAGCCG

19

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: genomic DNA
(iii) HYPOTHETICAL: no
(iv) ANTI-SENSE: no
(v) ORIGINAL SOURCE:
(A) ORGANISM: human
(ix) FEATURE:
(A) NAME/KEY: 144

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

TGGTCCCAAT ACTCAGGCCT

20

(2) INFORMATION FOR SEQ ID NO:228:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: genomic DNA
(iii) HYPOTHETICAL: no
(iv) ANTI-SENSE: no
(v) ORIGINAL SOURCE:
(A) ORGANISM: human
(ix) FEATURE:
(A) NAME/KEY: 145

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

GCAGGGTCCC CAGGTTCG

18

(2) INFORMATION FOR SEQ ID NO:229:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: 152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

GGGCCGCCTC CCAGTTGT

18

(2) INFORMATION FOR SEQ ID NO:230:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: 153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

TCTGTGAGTG GGCTACACA

20

(2) INFORMATION FOR SEQ ID NO:231:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: 154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

CCTTCACATT CCGTGTCTGC A

21

(2) INFORMATION FOR SEQ ID NO:232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: 155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

GAGCCACTCC ACGCACGT

18

(2) INFORMATION FOR SEQ ID NO:233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: 161

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

CCACTCGGTC AGTCTCTGAC

20

(2) INFORMATION FOR SEQ ID NO:234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: 165

140

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

GAGCGCAGGT CCTCGTTCAA

20

(2) INFORMATION FOR SEQ ID NO:235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (i) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: 168

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

GTCTGTGAGT GGGCCATCAT

20

(2) INFORMATION FOR SEQ ID NO:236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: 180

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

CAGCCATACA TCCTCAGGAC

20

(2) INFORMATION FOR SEQ ID NO:237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human

141

(ix) FEATURE:
(A) NAME/KEY: Ex2 (Aw3)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

GCGCCGGGAG GAGGGTC

17

(2) INFORMATION FOR SEQ ID NO:238:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA
(iii) HYPOTHETICAL: no
(iv) ANTI-SENSE: no
(v) ORIGINAL SOURCE:
(A) ORGANISM: human
(ix) FEATURE:
(A) NAME/KEY: Ex2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

ATCTCGGACC CGGAGACT

18

(2) INFORMATION FOR SEQ ID NO:239:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA
(iii) HYPOTHETICAL: no
(iv) ANTI-SENSE: no
(v) ORIGINAL SOURCE:
(A) ORGANISM: human
(ix) FEATURE:
(A) NAME/KEY: Ex3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

GTTTCATTT CAGTTAGGC CA

22

(2) INFORMATION FOR SEQ ID NO:240:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

142

- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: Ex3 (Aw6)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

CGGGAGATCT ACAGGGCGATC AGG

23

(2) INFORMATION FOR SEQ ID NO:241:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: Ex2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

GTCGTGACCT GCGCCCC

17

(2) INFORMATION FOR SEQ ID NO:242:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: Ex3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

GGGCGGGGCG GGGCTCGGG

19

(2) INFORMATION FOR SEQ ID NO:243:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: Ex2 (ABCw1)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

GGTCGTGACC TTCCGGCCCC

19

(2) INFORMATION FOR SEQ ID NO:244:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: Ex3 (ABCw2)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

CCCGGGTTTCA TTTTC

15

(2) INFORMATION FOR SEQ ID NO:245:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: 119

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

CTTCACATTC CGTGTCTCCT

20

WHAT IS CLAIMED IS:

1. A method of determining the HLA Class I group type of a subject comprising the following steps:

(i) combining a group-specific untranslated region primer pair with a target DNA sample from the subject under conditions such that primer-based amplification of the target DNA may occur; and

(ii) determining whether a nucleic acid product is produced by the amplification;

wherein the ability of the primer pair to produce a nucleic acid product is associated with a particular HLA group type.

2. The method of claim 1, wherein the HLA Class I group to be determined is part of the HLA-A locus.

3. The method of claim 1, further comprising the step of (iii) determining the nucleic acid sequence of the nucleic acid product of step (ii).

4. The method of claim 1, wherein the primer pair comprises one or more oligonucleotide primers selected from the group consisting of I1-210m (SEQ ID NO:35), I1-230m (SEQ ID NO:181), I1-226 (SEQ ID NO:182), I1-221m11 (SEQ ID NO:183), I1-209 (SEQ ID NO: 184), I1-214m (SEQ ID NO: 185), I1-223d (SEQ ID NO: 186), I1-225m (SEQ ID NO:187), I1-237m14 (SEQ ID NO:188), I1-240 (SEQ ID NO:189), 5'FL-243 (SEQ ID NO:190), 5'FR-257 (SEQ ID NO:191), 5'FR-273 (SEQ ID NO:192), BP202 (SEQ ID NO:193), BP203 (SEQ ID NO:194), BP142 (SEQ ID NO:195), I3-236 (SEQ ID NO:196), I3-239 (SEQ ID NO:197), I3-246 (SEQ ID NO:198), I3-247m6 (SEQ ID NO:199), I3-249 (SEQ ID NO:200), I3-280m18 (SEQ ID NO:201) and I3-282 (SEQ ID NO:202).

5. The method of claim 1, wherein the primer pair is selected from the group of pairs consisting of I1-230m (SEQ ID NO:181) and BP142 (SEQ ID NO:195); 5'FR-257 (SEQ ID NO:191) and I3-247m6 (SEQ ID NO:199); I1-230m (SEQ ID NO:181) and I3-247m6 (SEQ ID NO:199); I1-226 (SEQ ID NO:182) and I3-249 (SEQ ID NO:200); I1-221m11 (SEQ ID NO:183) and I3-280m18 (SEQ ID

NO:201); 5'FL-243 (SEQ ID NO:190) and I3-249 (SEQ ID NO:200); I1-214m (SEQ ID NO:185) and I3-249 (SEQ ID NO:200); I1-210m (SEQ ID NO:35) and I3-236 (SEQ ID NO:196); I1-210m (SEQ ID NO:35) and I3-249 (SEQ ID NO:200); 5'FR-273 (SEQ ID NO:192) and I3-249 (SEQ ID NO:200); I1-223d (SEQ ID NO:186) and I3-239 (SEQ ID NO:197); I1-223d (SEQ ID NO:186) and I3-249 (SEQ ID NO:200); I1-240 (SEQ ID NO:189) and I3-249 (SEQ ID NO:200); I1-237m14 (SEQ ID NO:188) and I3-249 (SEQ ID NO:200); I1-225m (SEQ ID NO:187) and I3-249 (SEQ ID NO:200); BP202 (SEQ ID NO:193) and I3-249 (SEQ ID NO:200) and BP203 (SEQ ID NO:194) and I3-282 (SEQ ID NO:202).

6. A method of determining the HLA Class I allele type of a subject comprising the following steps:

(i) combining a group-specific exon region primer pair with a target DNA sample from the subject under conditions such that primer-based amplification of the target DNA may occur;

(ii) determining whether a first nucleic acid product is produced by the amplification wherein the ability of the primer pair to produce a nucleic acid product is associated with a particular HLA group type, and thereby identifying the group type;

(iii) combining a group-specific untranslated region primer pair corresponding to the group type of the subject, as determined by steps (i)-(ii), with a target DNA sample from the subject under conditions such that primer-based amplification of the target DNA may occur and a second nucleic acid product is produced; and

(iv) determining the nucleic acid sequence of the second nucleic acid product collected in step (iii).

7. The method of claim 6, wherein the HLA Class I allele to be determined is part of the HLA-A locus.

8. The method of claim 6, wherein the group-specific exon region primer pair used in step (i) comprises one or more oligonucleotide primers selected

from the group consisting of primers 85 (SEQ ID NO:203), 118 (SEQ ID NO:204), 120 (SEQ ID NO:205), 123 (SEQ ID NO:206), 127 (SEQ ID NO:207), 129 (SEQ ID NO:208), 134 (SEQ ID NO:209), 137 (SEQ ID NO:210), 140 (SEQ ID NO:211), 160 (SEQ ID NO:212), 167 (SEQ ID NO:213), 175 (SEQ ID NO:214), 193 (SEQ ID NO:215), 202 (SEQ ID NO:216), 98 (SEQ ID NO:217), 115 (SEQ ID NO:218), 116 (SEQ ID NO:219), 117 (SEQ ID NO:220), 119 (SEQ ID NO:245), 126 (SEQ ID NO:221), 133 (SEQ ID NO:222), 135 (SEQ ID NO:223), 136 (SEQ ID NO:224), 138 (SEQ ID NO:225), 142 (SEQ ID NO:226), 144 (SEQ ID NO:227), 145 (SEQ ID NO:228), 152 (SEQ ID NO:229), 153 (SEQ ID NO:230), 154 (SEQ ID NO:231), 155 (SEQ ID NO:232), 161 (SEQ ID NO:233), 165 (SEQ ID NO:234), 168 (SEQ ID NO:235) and 180 (SEQ ID NO:236).

9. The method of claim 6, wherein the group-specific exon region primer pair used in step (i) is selected from the group of pairs consisting of 140 (SEQ ID NO:211) and 142 (SEQ ID NO:226); 85 (SEQ ID NO:203) and 98 (SEQ ID NO:217); 140 (SEQ ID NO:211) and 126 (SEQ ID NO:221); 167 (SEQ ID NO:213) and 168 (SEQ ID NO:235); 118 (SEQ ID NO:204) and 119 (SEQ ID NO:245); 129 (SEQ ID NO:208) and 115 (SEQ ID NO:218); 129 (SEQ ID NO:208) and 116 (SEQ ID NO:219) and 117 (SEQ ID NO:220); 160 (SEQ ID NO:212) and 135 (SEQ ID NO:223); 118 (SEQ ID NO:204) and 133 (SEQ ID NO:222); 118 (SEQ ID NO:204) and 145 (SEQ ID NO:228); 134 (SEQ ID NO:209) and 155 (SEQ ID NO:232); 134 (SEQ ID NO:209) and 136 (SEQ ID NO:224); 118 (SEQ ID NO:204) and 161 (SEQ ID NO:233); 118 (SEQ ID NO:204) and 154 (SEQ ID NO:231); 120 (SEQ ID NO:205) and 152 (SEQ ID NO:229); 193 (SEQ ID NO:215) and 180 (SEQ ID NO:236); 127 (SEQ ID NO:207) and 165 (SEQ ID NO:234); 137 (SEQ ID NO:210) and 145 (SEQ ID NO:228); 175 (SEQ ID NO:214) and 115 (SEQ ID NO:218) and 116 (SEQ ID NO:219); 167 (SEQ ID NO:213) and 144 (SEQ ID NO:227); 167 (SEQ ID NO:213) and 133 (SEQ ID NO:222); 137 (SEQ ID NO:210) and 138 (SEQ ID NO:225); 202 (SEQ ID NO:216) and 153 (SEQ ID NO:230); and 140 (SEQ ID NO:211) and 136 (SEQ ID NO:224).

10. The method of claim 6, wherein the group-specific untranslated region primer pair used in step (iii) comprises one or more oligonucleotide primers selected from the group consisting of I1-210m (SEQ ID NO:35), I1-230m (SEQ ID NO:181), I1-226 (SEQ ID NO:182), I1-221m11 (SEQ ID NO:183), I1-209 (SEQ ID NO: 184), I1-214m (SEQ ID NO: 185), I1-223d (SEQ ID NO: 186), I1-225m (SEQ ID NO:187), I1-237m14 (SEQ ID NO:188), I1-240 (SEQ ID NO:189), 5'FL-243 (SEQ ID NO:190), 5'FR-257 (SEQ ID NO:191), 5'FR-273 (SEQ ID NO:192), BP202 (SEQ ID NO:193), BP203 (SEQ ID NO:194), BP142 (SEQ ID NO:195), I3-236 (SEQ ID NO:196), I3-239 (SEQ ID NO:197), I3-246 (SEQ ID NO:198), I3-247m6 (SEQ ID NO:199), I3-249 (SEQ ID NO:200), I3-280m18 (SEQ ID NO:201) and I3-282 (SEQ ID NO:202).

11. The method of claim 6, wherein the group-specific untranslated region primer pair used in step (iii) is selected from the group of oligonucleotide primer pairs consisting of I1-230m (SEQ ID NO:181) and BP142 (SEQ ID NO:195); 5'FR-257 (SEQ ID NO:191) and I3-247m6 (SEQ ID NO:199); I1-230m (SEQ ID NO:181) and I3-247m6 (SEQ ID NO:199); I1-226 (SEQ ID NO:182) and I3-249 (SEQ ID NO:200); I1-221m11 (SEQ ID NO:183) and I3-280m18 (SEQ ID NO:201); 5'FL-243 (SEQ ID NO:190) and I3-249 (SEQ ID NO:200); I1-214m (SEQ ID NO:185) and I3-249 (SEQ ID NO:200); I1-210m (SEQ ID NO:35) and I3-236 (SEQ ID NO:196); I1-210m (SEQ ID NO:35) and I3-249 (SEQ ID NO:200); 5'FR-273 (SEQ ID NO:192) and I3-249 (SEQ ID NO:200); I1-223d (SEQ ID NO:186) and I3-239 (SEQ ID NO:197); I1-223d (SEQ ID NO:186) and I3-249 (SEQ ID NO:200); I1-240 (SEQ ID NO:189) and I3-249 (SEQ ID NO:200); I1-237m14 (SEQ ID NO:188) and I3-249 (SEQ ID NO:200); I1-225m (SEQ ID NO:187) and I3-249 (SEQ ID NO:200); BP202 (SEQ ID NO:193) and I3-249 (SEQ ID NO:200) and BP203 (SEQ ID NO:194) and I3-282 (SEQ ID NO:202).

12. A method of determining the HLA Class I allele type of a subject comprising the following steps:

(i) combining a plurality of group-specific exon region primer pairs

with a target DNA sample from the subject under conditions such that primer-based amplification of the target DNA may occur and a first nucleic acid product is produced;

(ii) determining the size of the first nucleic acid product of the amplification;

(iii) correlating the size of the first nucleic acid product with the predicted size of a fragment associated with a particular HLA type;

(iv) combining a group-specific untranslated region primer pair corresponding to the group type of the subject, as determined by steps (i)-(iii), with a target DNA sample from the subject under conditions such that primer-based amplification of the target DNA may occur and a second nucleic acid product is produced; and

(v) determining the nucleic acid sequence of the second nucleic acid product.

13. The method of claim 12, wherein the HLA Class I allele to be determined is part of the HLA-A locus.

14. The method of claim 12, wherein the plurality of group-specific exon region primer pairs used in step (i) comprises one or more oligonucleotide primers selected from the group consisting of primers 85 (SEQ ID NO:203), 118 (SEQ ID NO:204), 120 (SEQ ID NO:205), 123 (SEQ ID NO:206), 127 (SEQ ID NO:207), 129 (SEQ ID NO:208), 134 (SEQ ID NO:209), 137 (SEQ ID NO:210), 140 (SEQ ID NO:211), 160 (SEQ ID NO:212), 167 (SEQ ID NO:213), 175 (SEQ ID NO:214), 193 (SEQ ID NO:215), 202 (SEQ ID NO:216), 98 (SEQ ID NO:217), 115 (SEQ ID NO:218), 116 (SEQ ID NO:219), 117 (SEQ ID NO:220), 126 (SEQ ID NO:221), 133 (SEQ ID NO:222), 135 (SEQ ID NO:223), 136 (SEQ ID NO:224), 138 (SEQ ID NO:225), 142 (SEQ ID NO:226), 144 (SEQ ID NO:227), 145 (SEQ ID NO:228), 152 (SEQ ID NO:229), 153 (SEQ ID NO:230), 154 (SEQ ID NO:231), 155 (SEQ ID NO:232), 161 (SEQ ID NO:233), 165 (SEQ ID NO:234), 168 (SEQ ID NO:235) and 180 (SEQ ID NO:236).

15. The method of claim 12, wherein the plurality of group-specific exon region primer pairs used in step (i) comprises one or more oligonucleotide primer pairs selected from the group of pairs consisting of 140 (SEQ ID NO:211) and 142 (SEQ ID NO:226); 85 (SEQ ID NO:203) and 98 (SEQ ID NO:217); 140 (SEQ ID NO:211) and 126 (SEQ ID NO:221); 167 (SEQ ID NO:213) and 168 (SEQ ID NO:235); 118 (SEQ ID NO:204) and 119 (SEQ ID NO:245); 129 (SEQ ID NO:208) and 115 (SEQ ID NO:218); 129 (SEQ ID NO:208) and 116 (SEQ ID NO:219) and 117 (SEQ ID NO:220); 160 (SEQ ID NO:212) and 135 (SEQ ID NO:223); 118 (SEQ ID NO:204) and 133 (SEQ ID NO:222); 118 (SEQ ID NO:204) and 145 (SEQ ID NO:228); 134 (SEQ ID NO:209) and 155 (SEQ ID NO:232); 134 (SEQ ID NO:209) and 136 (SEQ ID NO:224); 118 (SEQ ID NO:204) and 161 (SEQ ID NO:233); 118 (SEQ ID NO:204) and 154 (SEQ ID NO:231); 120 (SEQ ID NO:205) and 152 (SEQ ID NO:229); 193 (SEQ ID NO:215) and 180 (SEQ ID NO:236); 127 (SEQ ID NO:207) and 165 (SEQ ID NO:234); 137 (SEQ ID NO:210) and 145 (SEQ ID NO:228); 175 (SEQ ID NO:214) and 115 (SEQ ID NO:218) and 116 (SEQ ID NO:219); 167 (SEQ ID NO:213) and 144 (SEQ ID NO:227); 167 (SEQ ID NO:213) and 133 (SEQ ID NO:222); 137 (SEQ ID NO:210) and 138 (SEQ ID NO:225); 202 (SEQ ID NO:216) and 153 (SEQ ID NO:230); and 140 (SEQ ID NO:211) and 136 (SEQ ID NO:224).

16. The method of claim 12, wherein the group-specific untranslated region primer pair used in step (iv) comprises one or more oligonucleotide primers selected from the group consisting of I1-210m (SEQ ID NO:35), I1-230m (SEQ ID NO:181), I1-226 (SEQ ID NO:182), I1-221m11 (SEQ ID NO:183), I1-209 (SEQ ID NO:184), I1-214m (SEQ ID NO:185), I1-223d (SEQ ID NO:186), I1-225m (SEQ ID NO:187), I1-237m14 (SEQ ID NO:188), I1-240 (SEQ ID NO:189), 5'FL-243 (SEQ ID NO:190), 5'FR-257 (SEQ ID NO:191), 5'FR-273 (SEQ ID NO:192), BP202 (SEQ ID NO:193), BP203 (SEQ ID NO:194), BP142 (SEQ ID NO:195), I3-236 (SEQ ID NO:196), I3-239 (SEQ ID NO:197), I3-246 (SEQ ID NO:198), I3-247m6 (SEQ ID NO:199), I3-249 (SEQ ID NO:200), I3-280m18 (SEQ ID NO:201) and I3-282 (SEQ

ID NO:202).

17. The method of claim 12, wherein the group-specific untranslated region primer pair used in step (iv) is selected from the group of oligonucleotide primer pairs consisting of I1-230m (SEQ ID NO:181) and BP142 (SEQ ID NO:195); 5'FR-257 (SEQ ID NO:191) and I3-247m6 (SEQ ID NO:199); I1-230m (SEQ ID NO:181) and I3-247m6 (SEQ ID NO:199); I1-226 (SEQ ID NO:182) and I3-249 (SEQ ID NO:200); I1-221m11 (SEQ ID NO:183) and I3-280m18 (SEQ ID NO:201); 5'FL-243 (SEQ ID NO:190) and I3-249 (SEQ ID NO:200); I1-214m (SEQ ID NO:185) and I3-249 (SEQ ID NO:200); I1-210m (SEQ ID NO:35) and I3-236 (SEQ ID NO:196); I1-210m (SEQ ID NO:35) and I3-249 (SEQ ID NO:200); 5'FR-273 (SEQ ID NO:192) and I3-249 (SEQ ID NO:200); I1-223d (SEQ ID NO:186) and I3-239 (SEQ ID NO:197); I1-223d (SEQ ID NO:186) and I3-249 (SEQ ID NO:200); I1-240 (SEQ ID NO:189) and I3-249 (SEQ ID NO:200); I1-237m14 (SEQ ID NO:188) and I3-249 (SEQ ID NO:200); I1-225m (SEQ ID NO:187) and I3-249 (SEQ ID NO:200); BP202 (SEQ ID NO:193) and I3-249 (SEQ ID NO:200) and BP203 (SEQ ID NO:194) and I3-282 (SEQ ID NO:202).

18. A composition comprising a plurality of oligonucleotide primer pairs comprising one or more primers selected from the group consisting of I1-210m (SEQ ID NO:35), I1-230m (SEQ ID NO:181), I1-226 (SEQ ID NO:182), I1-221m11 (SEQ ID NO:183), I1-209 (SEQ ID NO: 184), I1-214m (SEQ ID NO: 185), I1-223d (SEQ ID NO: 186), I1-225m (SEQ ID NO:187), I1-237m14 (SEQ ID NO:188), I1-240 (SEQ ID NO:189), 5'FL-243 (SEQ ID NO:190), 5'FR-257 (SEQ ID NO:191), 5'FR-273 (SEQ ID NO:192), BP202 (SEQ ID NO:193), BP203 (SEQ ID NO:194), BP142 (SEQ ID NO:195), I3-236 (SEQ ID NO:196), I3-239 (SEQ ID NO:197), I3-246 (SEQ ID NO:198), I3-247m6 (SEQ ID NO:199), I3-249 (SEQ ID NO:200), I3-280m18 (SEQ ID NO:201) and I3-282 (SEQ ID NO:202).

19. A composition comprising an oligonucleotide primer selected from the group consisting of I1-210m (SEQ ID NO:35), I1-230m (SEQ ID NO:181), I1-226 (SEQ ID NO:182), I1-221m11 (SEQ ID NO:183), I1-209 (SEQ ID NO: 184), I1-

214m (SEQ ID NO: 185), I1-223d (SEQ ID NO: 186), I1-225m (SEQ ID NO:187), I1-237m14 (SEQ ID NO:188), I1-240 (SEQ ID NO:189), 5'FL-243 (SEQ ID NO:190), 5'FR-257 (SEQ ID NO:191), 5'FR-273 (SEQ ID NO:192), BP202 (SEQ ID NO:193), BP203 (SEQ ID NO:194), BP142 (SEQ ID NO:195), I3-236 (SEQ ID NO:196), I3-239 (SEQ ID NO:197), I3-246 (SEQ ID NO:198), I3-247m6 (SEQ ID NO:199), I3-249 (SEQ ID NO:200), I3-280m18 (SEQ ID NO:201) and I3-282 (SEQ ID NO:202).

20. A composition comprising an oligonucleotide primer pair selected from the group consisting of I1-230m (SEQ ID NO:181) and BP142 (SEQ ID NO:195); 5'FR-257 (SEQ ID NO:191) and I3-247m6 (SEQ ID NO:199); I1-230m (SEQ ID NO:181) and I3-247m6 (SEQ ID NO:199); I1-226 (SEQ ID NO:182) and I3-249 (SEQ ID NO:200); I1-221m11 (SEQ ID NO:183) and I3-280m18 (SEQ ID NO:201); 5'FL-243 (SEQ ID NO:190) and I3-249 (SEQ ID NO:200); I1-214m (SEQ ID NO:185) and I3-249 (SEQ ID NO:200); I1-210m (SEQ ID NO:35) and I3-236 (SEQ ID NO:196); I1-210m (SEQ ID NO:35) and I3-249 (SEQ ID NO:200); 5'FR-273 (SEQ ID NO:192) and I3-249 (SEQ ID NO:200); I1-223d (SEQ ID NO:186) and I3-239 (SEQ ID NO:197); I1-223d (SEQ ID NO:186) and I3-249 (SEQ ID NO:200); I1-240 (SEQ ID NO:189) and I3-249 (SEQ ID NO:200); I1-237m14 (SEQ ID NO:188) and I3-249 (SEQ ID NO:200); I1-225m (SEQ ID NO:187) and I3-249 (SEQ ID NO:200); BP202 (SEQ ID NO:193) and I3-249 (SEQ ID NO:200) and BP203 (SEQ ID NO:194) and I3-282 (SEQ ID NO:202).

21. A kit comprising:

(a) a plurality of oligonucleotide group-specific untranslated region primer pairs comprising one or more primers selected from the group consisting of I1-210m (SEQ ID NO:35), I1-230m (SEQ ID NO:181), I1-226 (SEQ ID NO:182), I1-221m11 (SEQ ID NO:183), I1-209 (SEQ ID NO: 184), I1-214m (SEQ ID NO: 185), I1-223d (SEQ ID NO: 186), I1-225m (SEQ ID NO:187), I1-237m14 (SEQ ID NO:188), I1-240 (SEQ ID NO:189), 5'FL-243 (SEQ ID NO:190), 5'FR-257 (SEQ ID NO:191), 5'FR-273 (SEQ ID NO:192), BP202 (SEQ ID NO:193), BP203 (SEQ ID

NO:194), BP142 (SEQ ID NO:195), I3-236 (SEQ ID NO:196), I3-239 (SEQ ID NO:197), I3-246 (SEQ ID NO:198), I3-247m6 (SEQ ID NO:199), I3-249 (SEQ ID NO:200), I3-280m18 (SEQ ID NO:201) and I3-282 (SEQ ID NO:202); and

(b) an enzyme for nucleotide chain extension.

22. A kit comprising:

(a) an oligonucleotide group-specific untranslated region primer selected from the group consisting of I1-210m (SEQ ID NO:35), I1-230m (SEQ ID NO:181), I1-226 (SEQ ID NO:182), I1-221m11 (SEQ ID NO:183), I1-209 (SEQ ID NO: 184), I1-214m (SEQ ID NO: 185), I1-223d (SEQ ID NO: 186), I1-225m (SEQ ID NO:187), I1-237m14 (SEQ ID NO:188), I1-240 (SEQ ID NO:189), 5'FL-243 (SEQ ID NO:190), 5'FR-257 (SEQ ID NO:191), 5'FR-273 (SEQ ID NO:192), BP202 (SEQ ID NO:193), BP203 (SEQ ID NO:194), BP142 (SEQ ID NO:195), I3-236 (SEQ ID NO:196), I3-239 (SEQ ID NO:197), I3-246 (SEQ ID NO:198), I3-247m6 (SEQ ID NO:199), I3-249 (SEQ ID NO:200), I3-280m18 (SEQ ID NO:201) and I3-282 (SEQ ID NO:202); and

(b) an enzyme for nucleotide chain extension.

23. The kit of claim 22, further comprising:

(c) a cocktail comprising group-specific exon region primers comprising one or more primer selected from the group consisting of 85 (SEQ ID NO:203), 118 (SEQ ID NO:204), 120 (SEQ ID NO:205), 123 (SEQ ID NO:206), 127 (SEQ ID NO:207), 129 (SEQ ID NO:208), 134 (SEQ ID NO:209), 137 (SEQ ID NO:210), 140 (SEQ ID NO:211), 160 (SEQ ID NO:212), 167 (SEQ ID NO:213), 175 (SEQ ID NO:214), 193 (SEQ ID NO:215), 202 (SEQ ID NO:216), 98 (SEQ ID NO:217), 115 (SEQ ID NO:218), 116 (SEQ ID NO:219), 117 (SEQ ID NO:220), 126 (SEQ ID NO:221), 133 (SEQ ID NO:222), 135 (SEQ ID NO:223), 136 (SEQ ID NO:224), 138 (SEQ ID NO:225), 142 (SEQ ID NO:226), 144 SEQ ID NO:227), 145 (SEQ ID NO:228), 152 (SEQ ID NO:229), 153 SEQ ID NO:230), 154 (SEQ ID NO:231), 155 (SEQ ID NO:232), 161 (SEQ ID NO:233), 165 (SEQ ID NO:234), 168 (SEQ ID NO:235) and 180 (SEQ ID NO:236).

24. A kit comprising:

(a) an oligonucleotide primer pair selected from the group consisting of

I1-230m (SEQ ID NO:181) and BP142 (SEQ ID NO:195); 5'FR-257 (SEQ ID NO:191) and I3-247m6 (SEQ ID NO:199); I1-230m (SEQ ID NO:181) and I3-247m6 (SEQ ID NO:199); I1-226 (SEQ ID NO:182) and I3-249 (SEQ ID NO:200); I1-221m11 (SEQ ID NO:183) and I3-280m18 (SEQ ID NO:201); 5'FL-243 (SEQ ID NO:190) and I3-249 (SEQ ID NO:200); I1-214m (SEQ ID NO:185) and I3-249 (SEQ ID NO:200); I1-210m (SEQ ID NO:35) and I3-236 (SEQ ID NO:196); I1-210m (SEQ ID NO:35) and I3-249 (SEQ ID NO:200); 5'FR-273 (SEQ ID NO:192) and I3-249 (SEQ ID NO:200); I1-223d (SEQ ID NO:186) and I3-239 (SEQ ID NO:197); I1-223d (SEQ ID NO:186) and I3-249 (SEQ ID NO:200); I1-240 (SEQ ID NO:189) and I3-249 (SEQ ID NO:200); I1-237m14 (SEQ ID NO:188) and I3-249 (SEQ ID NO:200); I1-225m (SEQ ID NO:187) and I3-249 (SEQ ID NO:200); BP202 (SEQ ID NO:193) and I3-249 (SEQ ID NO:200) and BP203 (SEQ ID NO:194) and I3-282 (SEQ ID NO:202); and

(b) an enzyme for nucleotide chain extension..

25. The kit of claim 24, further comprising:

(c) a cocktail comprising group-specific exon region primers comprising one or more primer selected from the group consisting of 85 (SEQ ID NO:203), 118 (SEQ ID NO:204), 120 (SEQ ID NO:205), 123 (SEQ ID NO:206), 127 (SEQ ID NO:207), 129 (SEQ ID NO:208), 134 (SEQ ID NO:209), 137 (SEQ ID NO:210), 140 (SEQ ID NO:211), 160 (SEQ ID NO:212), 167 (SEQ ID NO:213), 175 (SEQ ID NO:214), 193 (SEQ ID NO:215), 202 (SEQ ID NO:216), 98 (SEQ ID NO:217), 115 (SEQ ID NO:218), 116 (SEQ ID NO:219), 117 (SEQ ID NO:220), 126 (SEQ ID NO:221), 133 (SEQ ID NO:222), 135 (SEQ ID NO:223), 136 (SEQ ID NO:224), 138 (SEQ ID NO:225), 142 (SEQ ID NO:226), 144 (SEQ ID NO:227), 145 (SEQ ID NO:228), 152 (SEQ ID NO:229), 153 (SEQ ID NO:230), 154 (SEQ ID NO:231), 155 (SEQ ID NO:232), 161 (SEQ ID NO:233), 165 (SEQ ID NO:234), 168

(SEQ ID NO:235) and 180 (SEQ ID NO:236).

(b) an enzyme for nucleotide chain extension..

26. The kit of claim 25, further comprising:

(d) a sequencing primer selected from the group consisting of 5'-

EX2(Aw3) 5' GCG GCG GGA GGA GGG TC 3' (SEQ ID NO:237), 3'-Ex2 5' ATC
TCG GAC CCG GAG ACT 3' (SEQ ID NO:238), 5' GTT TCA TTT TCA GTT TAG
GCC A 3' (SEQ ID NO:239), 3'-Ex3 (Aw6) 5' CGG GAG ATC TAC AGG CGA
TCA GG 3' (SEQ ID NO:241), 5'-Ex3 5' GGG CGG GGC GGG GCT CGG G 3
(SEQ ID NO:242), 3'-Ex2 (ABCw1) 5' GGT CGT GAC CT(T/C)CGC CCC 3' (SEQ
ID NO:243), and 5'-Ex3 (ABCw2) 5' CCC GGT TTC ATT TTC 3' (SEQ ID
NO:244).

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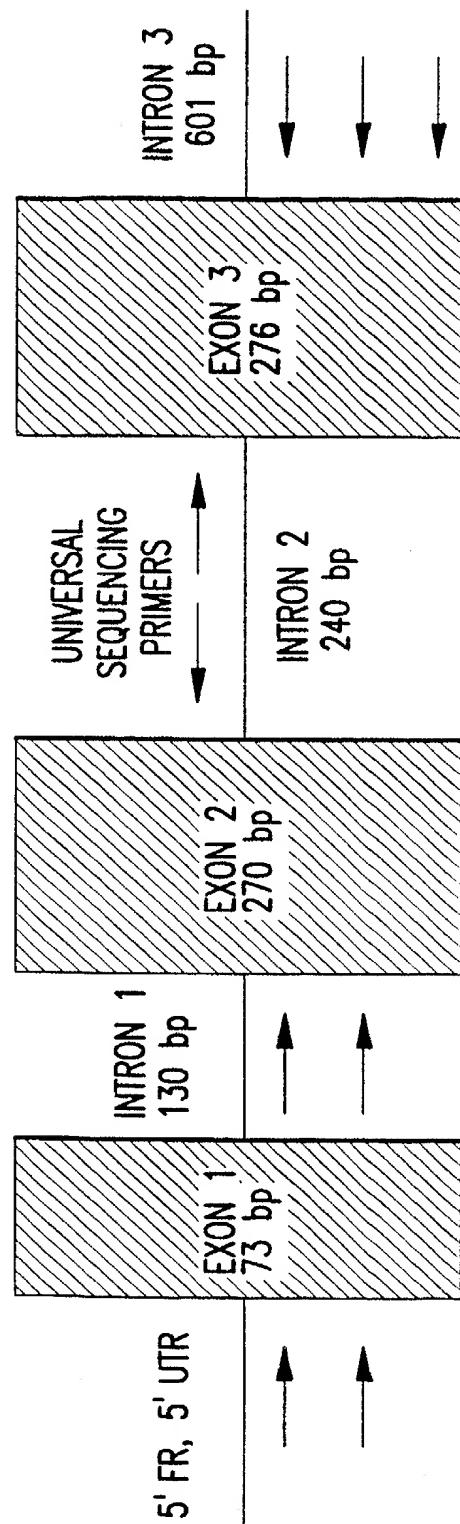


FIG. 1

GROUP-SPECIFIC NON-CODING REGION PRIMERS

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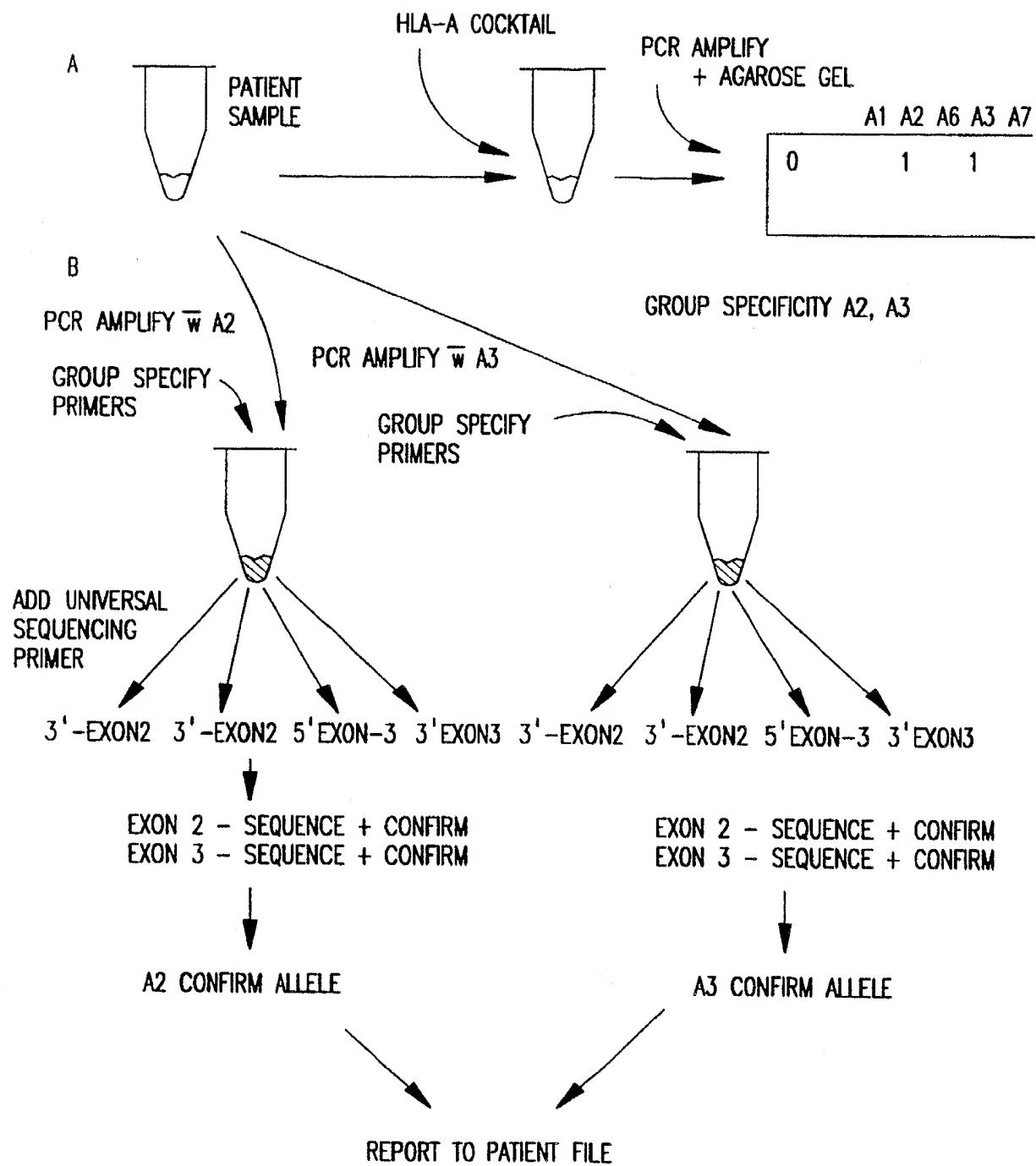


FIG.2(1)

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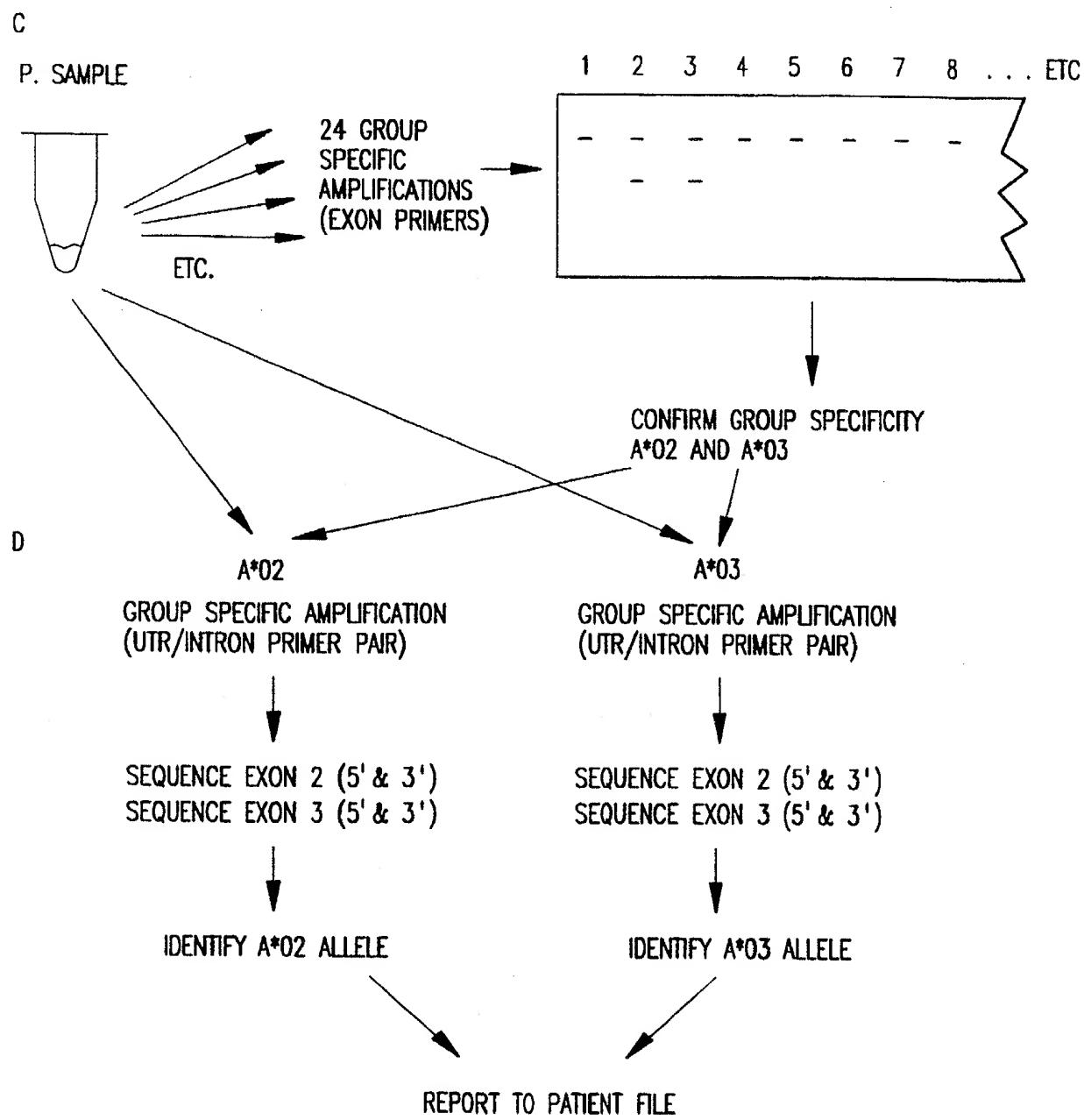
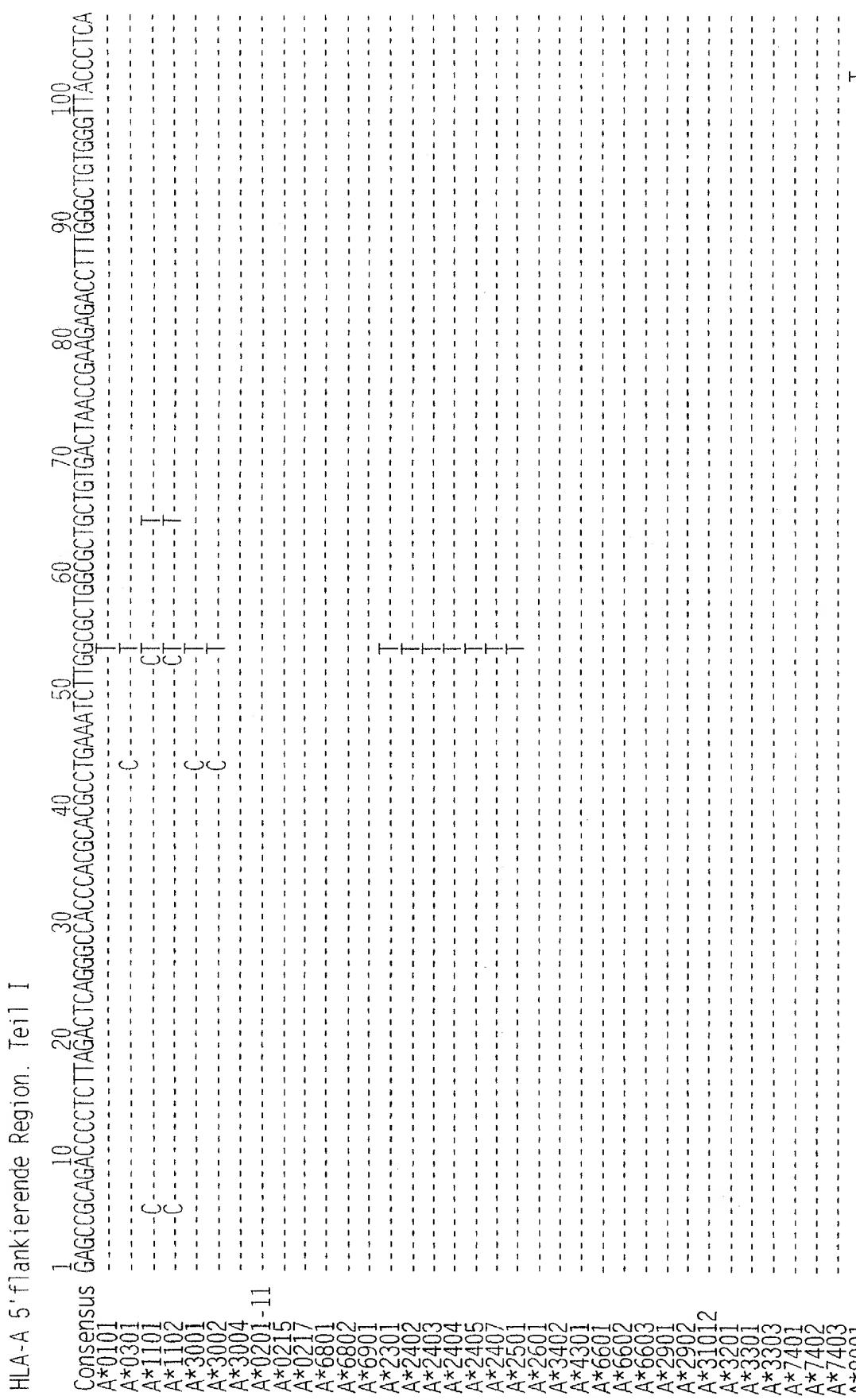


FIG.2(2)

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FIG. 3A

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HLA-A 5' flankierende Region, Teil II

Gonsensus	110	120	130	140	150	160	170	180	190	200
	CTCTGACCCAGGCCAGCACTATAGGTCTTCTGGATGATCCAAACCCCTAACGGCTTACGGGTTCCGACC									
A*0101										
A*0301										
A*1101										
A*1102										
A*3001										
A*3002										
A*3004										
A*0201-11										
A*0215										
A*0217										
A*66801										
A*66802										
A*6901										
A*2301										
A*2402										
A*2403										
A*2404										
A*2405										
A*2407										
A*2501										
A*2601										
A*3402										
A*4301										
A*6601										
A*6602										
A*6603										
A*2901										
A*2902										
A*31012										
A*3201										
A*3301										
A*3303										
A*7401										
A*7402										
A*7403										
A*8001										

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HLA-A 5' flankierende Region. Teil III

210 C₁GAGGGTTAGGTATGGGAAAGCCCCGGACTCTGGGACTCTCGGTGGACCCCTGAAGGAGCAGGACACGGTTGC
 220 C₁UUCUUCUUC
 230 C₁UUCUUCUUC
 240 C₁UUCUUCUUC
 250 C₁UUCUUCUUC
 260 C₁UUCUUCUUC
 270 C₁UUCUUCUUC
 280 C₁UUCUUCUUC
 290 C₁UUCUUCUUC
 300 C₁UUCUUCUUC

 Gconsensus
 A*0101
 A*1101
 A*1102
 A*3001
 A*3002
 A*3004
 A*0201-11
 A*0215
 A*0217
 A*6801
 A*6802
 A*6901
 A*2301
 A*2402
 A*2403
 A*2404
 A*2405
 A*2407
 A*2501
 A*2601
 A*3402
 A*4301
 A*6601
 A*6602
 A*6603
 A*2901
 A*2902
 A*3101₂
 A*3201
 A*3301
 A*3303
 A*7401
 A*7402
 A*7403
 A*8001

EIG. 3C

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HLA-A 5' flankierende Region, Teil IV

Gonsensus	310	320	330	340	350	360	370	380	390	400
	GAGACAGGTTACAGAGGACTAGAACCGGTTCTGAGACTCTTGTTCCTCTT									
A*0101										
A*0301										
A*1101										
A*1102										
A*30002										
A*30004-11										
A*0201										
A*0215										
A*0217										
A*6801										
A*6802										
A*6804										
A*6901										
A*2302										
A*2403										
A*2404										
A*2405										
A*2407										
A*2501										
A*2601										
A*3402										
A*4301										
A*6601										
A*6602										
A*6603										
A*2901										
A*2902										
A*31012										
A*3201										
A*3303										
A*3304										
A*7401										
A*7402										
A*7403										
A*8001										

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FIG. 3D

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HLA-A 5' flankierende Region, Teil V

	410	420	430	440	450
Gonsensus	TAGGGCATTAGAGACAGGGACTTGACTGAGGGACTGAGGGTG				
A*0101	-T-A-	-T-A-	-T-A-	-T-A-	-T-A-
A*0301	-T-A-	-T-A-	-T-A-	-T-A-	-T-A-
A*1101	-T-A-	-T-A-	-T-A-	-T-A-	-T-A-
A*1102	-T-A-	-T-A-	-T-A-	-T-A-	-T-A-
A*3001	-T-A-	-T-A-	-T-A-	-T-A-	-T-A-
A*3002	-T-A-	-T-A-	-T-A-	-T-A-	-T-A-
A*3004	-T-A-	-T-A-	-T-A-	-T-A-	-T-A-
A*020111	-T-A-	-T-A-	-T-A-	-T-A-	-T-A-
A*0215	-T-A-	-T-A-	-T-A-	-T-A-	-T-A-
A*0217	-T-A-	-T-A-	-T-A-	-T-A-	-T-A-
A*6801	-T-A-	-T-A-	-T-A-	-T-A-	-T-A-
A*6802	-T-A-	-T-A-	-T-A-	-T-A-	-T-A-
A*5901	-T-A-	-T-A-	-T-A-	-T-A-	-T-A-
A*2301	-T-A-	-T-A-	-T-A-	-T-A-	-T-A-
A*2402	-T-A-	-T-A-	-T-A-	-T-A-	-T-A-
A*2403	-T-A-	-T-A-	-T-A-	-T-A-	-T-A-
A*2404	-T-A-	-T-A-	-T-A-	-T-A-	-T-A-
A*2405	-T-A-	-T-A-	-T-A-	-T-A-	-T-A-
A*2407	-T-A-	-T-A-	-T-A-	-T-A-	-T-A-
A*2501	-T-A-	-T-A-	-T-A-	-T-A-	-T-A-
A*2503	-T-A-	-T-A-	-T-A-	-T-A-	-T-A-
A*2601	-T-A-	-T-A-	-T-A-	-T-A-	-T-A-
A*3402	-T-A-	-T-A-	-T-A-	-T-A-	-T-A-
A*4301	-T-A-	-T-A-	-T-A-	-T-A-	-T-A-
A*6601	-T-A-	-T-A-	-T-A-	-T-A-	-T-A-
A*6602	-T-A-	-T-A-	-T-A-	-T-A-	-T-A-
A*6603	-T-A-	-T-A-	-T-A-	-T-A-	-T-A-
A*2901	-T-A-	-T-A-	-T-A-	-T-A-	-T-A-
A*2902	-T-A-	-T-A-	-T-A-	-T-A-	-T-A-
A*31012	-T-A-	-T-A-	-T-A-	-T-A-	-T-A-
A*3201	-T-A-	-T-A-	-T-A-	-T-A-	-T-A-
A*3301	-T-A-	-T-A-	-T-A-	-T-A-	-T-A-
A*3303	-T-A-	-T-A-	-T-A-	-T-A-	-T-A-
A*7401	-T-A-	-T-A-	-T-A-	-T-A-	-T-A-
A*7402	-T-A-	-T-A-	-T-A-	-T-A-	-T-A-
A*7403	-T-A-	-T-A-	-T-A-	-T-A-	-T-A-
A*8001	-T-A-	-T-A-	-T-A-	-T-A-	-T-A-

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Consensus	1	10	20	30	40	50	60	70	80	90	100	110	120	130
A*0101	G	G	G	G	G	G	G	G	G	G	G	G	G	G
A*0301	C	C	C	C	C	C	C	C	C	C	C	C	C	C
A*1101	C	C	C	C	C	C	C	C	C	C	C	C	C	C
A*1102	C	C	C	C	C	C	C	C	C	C	C	C	C	C
A*3001	C	C	C	C	C	C	C	C	C	C	C	C	C	C
A*3002	C	C	C	C	C	C	C	C	C	C	C	C	C	C
A*3004	C	C	C	C	C	C	C	C	C	C	C	C	C	C
A*0201	C	C	C	C	C	C	C	C	C	C	C	C	C	C
A*0202	C	C	C	C	C	C	C	C	C	C	C	C	C	C
A*0203	C	C	C	C	C	C	C	C	C	C	C	C	C	C
A*0204	C	C	C	C	C	C	C	C	C	C	C	C	C	C
A*0205	C	C	C	C	C	C	C	C	C	C	C	C	C	C
A*0206	C	C	C	C	C	C	C	C	C	C	C	C	C	C
A*0207	C	C	C	C	C	C	C	C	C	C	C	C	C	C
A*0208	C	C	C	C	C	C	C	C	C	C	C	C	C	C
A*0209	C	C	C	C	C	C	C	C	C	C	C	C	C	C
A*0210	C	C	C	C	C	C	C	C	C	C	C	C	C	C
A*0211	C	C	C	C	C	C	C	C	C	C	C	C	C	C
A*0215	C	C	C	C	C	C	C	C	C	C	C	C	C	C
A*0217	C	C	C	C	C	C	C	C	C	C	C	C	C	C

FIG. 4A

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A 10x10 grid of dashed lines. The grid consists of 9 horizontal rows and 9 vertical columns, creating a pattern of 81 squares. Each square is defined by a dashed line on each of its four sides. In the center of each square, there is a small black square. In some of these central squares, there is additional text: the letters 'A' are placed in the squares at (1,1), (1,3), (1,5), (1,7), (1,9), (3,1), (3,3), (3,5), (3,7), (3,9), (5,1), (5,3), (5,5), (5,7), (5,9), (7,1), (7,3), (7,5), (7,7), (7,9), and (9,1). The letter 'x' is placed in the squares at (2,2), (2,4), (2,6), (2,8), (2,10), (4,2), (4,4), (4,6), (4,8), (4,10), (6,2), (6,4), (6,6), (6,8), (6,10), (8,2), (8,4), (8,6), (8,8), and (8,10). The squares at (0,0), (0,2), (0,4), (0,6), (0,8), (0,10), (2,0), (4,0), (6,0), (8,0), (10,0), (0,1), (2,1), (4,1), (6,1), (8,1), (1,2), (1,4), (1,6), (1,8), (1,10), (2,1), (4,1), (6,1), (8,1), (10,1), (2,0), (4,0), (6,0), (8,0), and (10,0) are empty.

A#6801	A#6802	A#6901	A#2301	A#2402	A#2403	A#2404	A#2405	A#2407	A#2501	A#2601	A#3402	A#6601	A#6602	A#6603	A#4301	A#2901	A#2902	A#3101	A#3201	A#3301	A#3303	A#7401	A#7403	A#8001
--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------

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FIG. 4B

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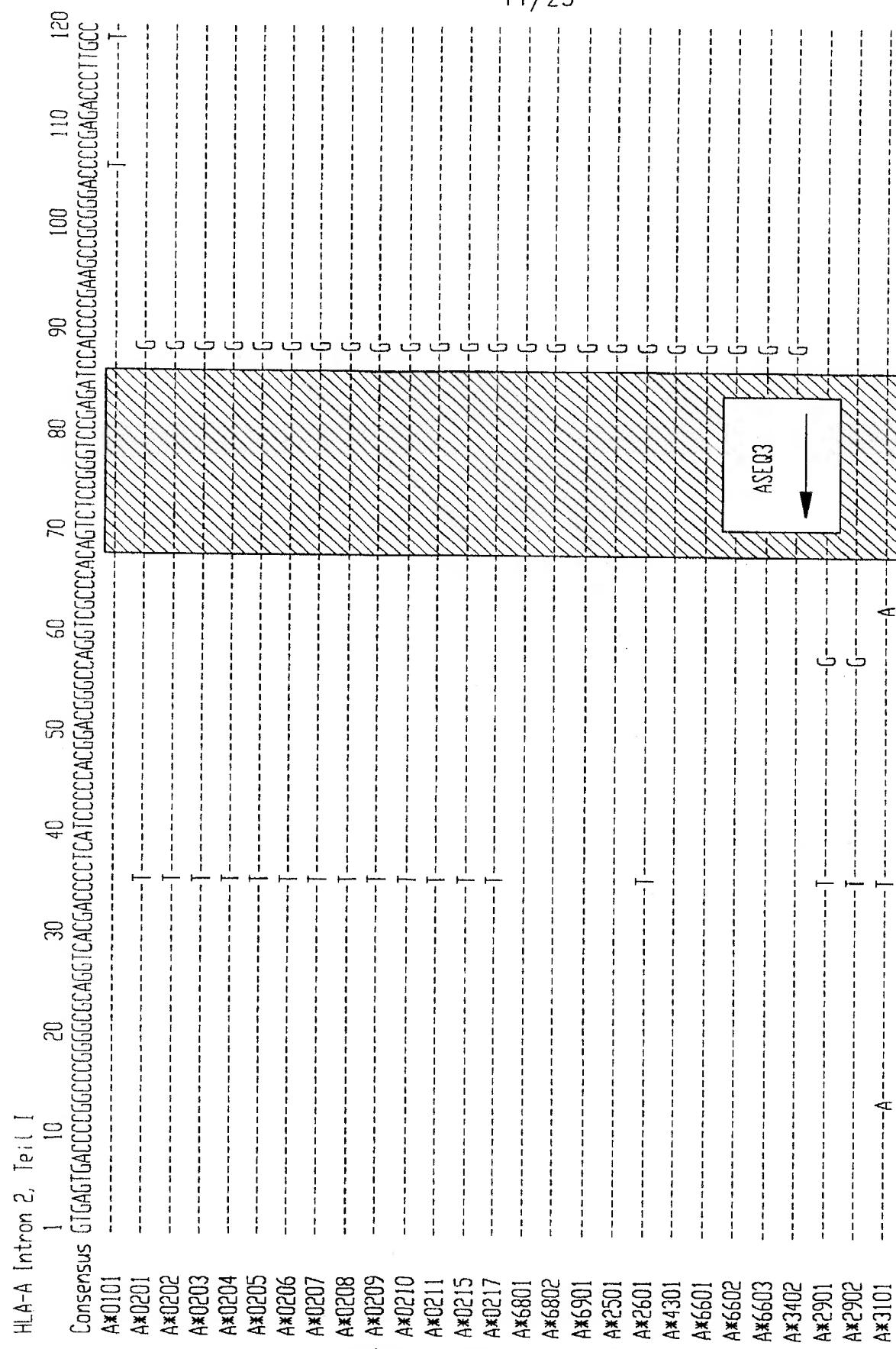
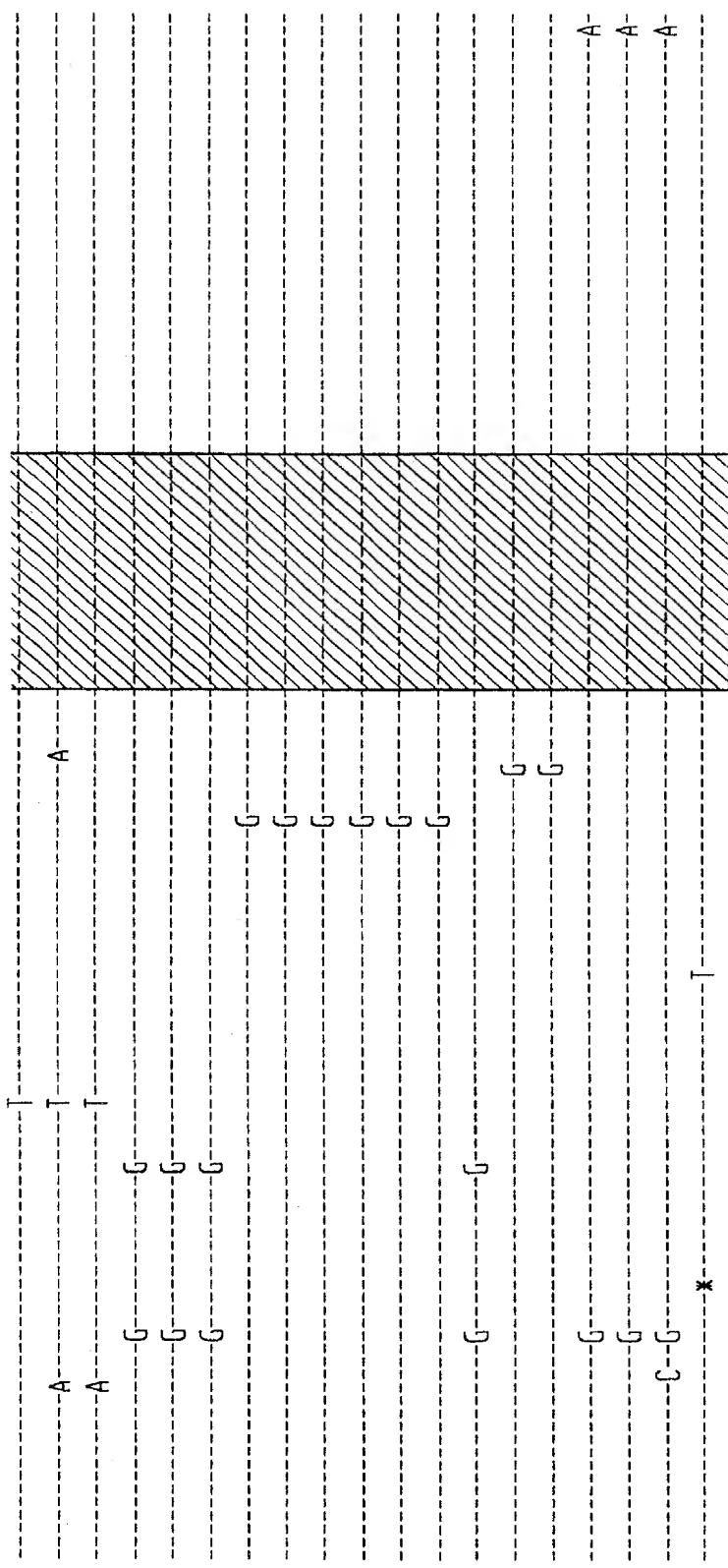


FIG. 5A

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FIG. 5B

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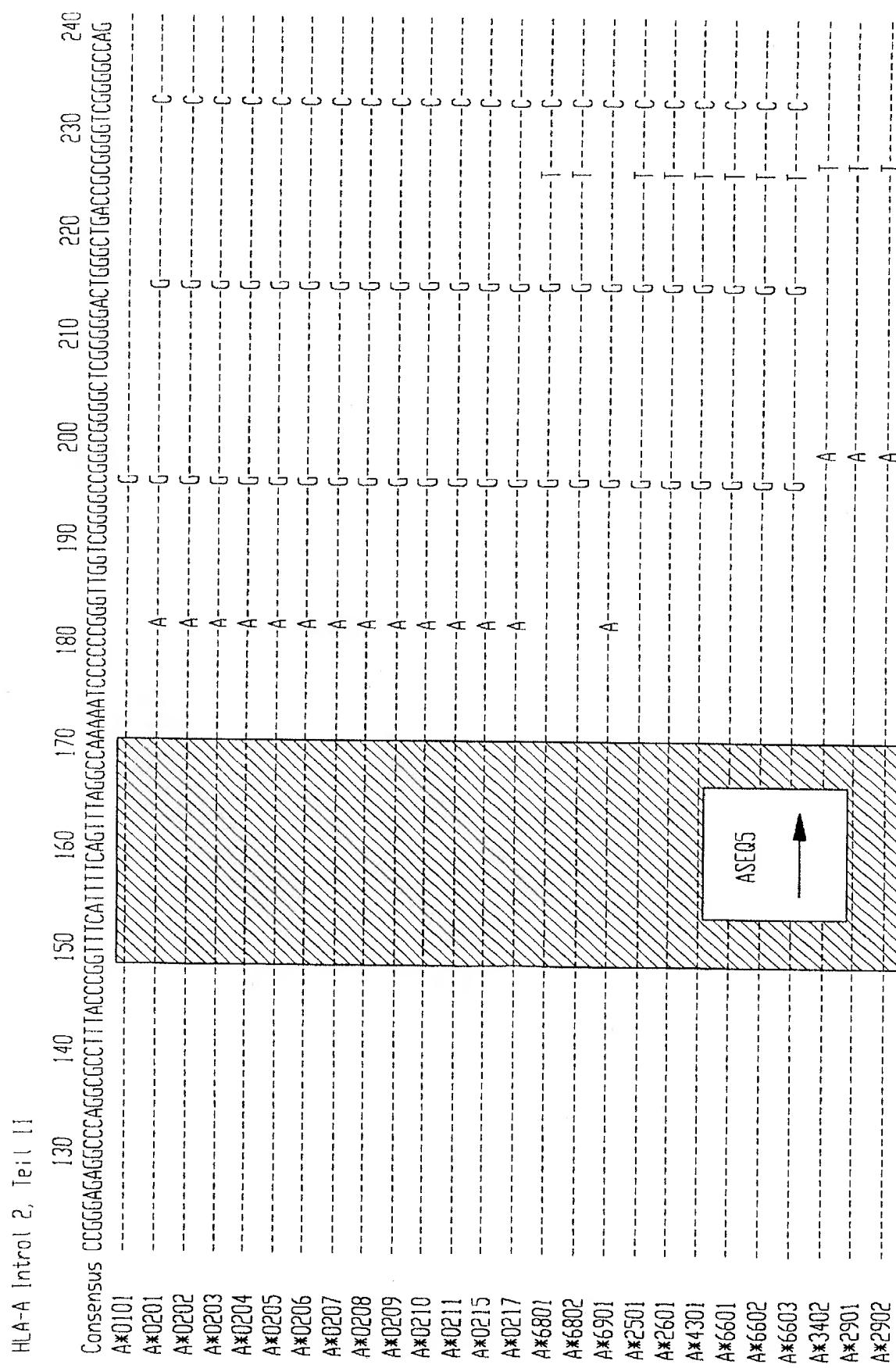


FIG. 5C

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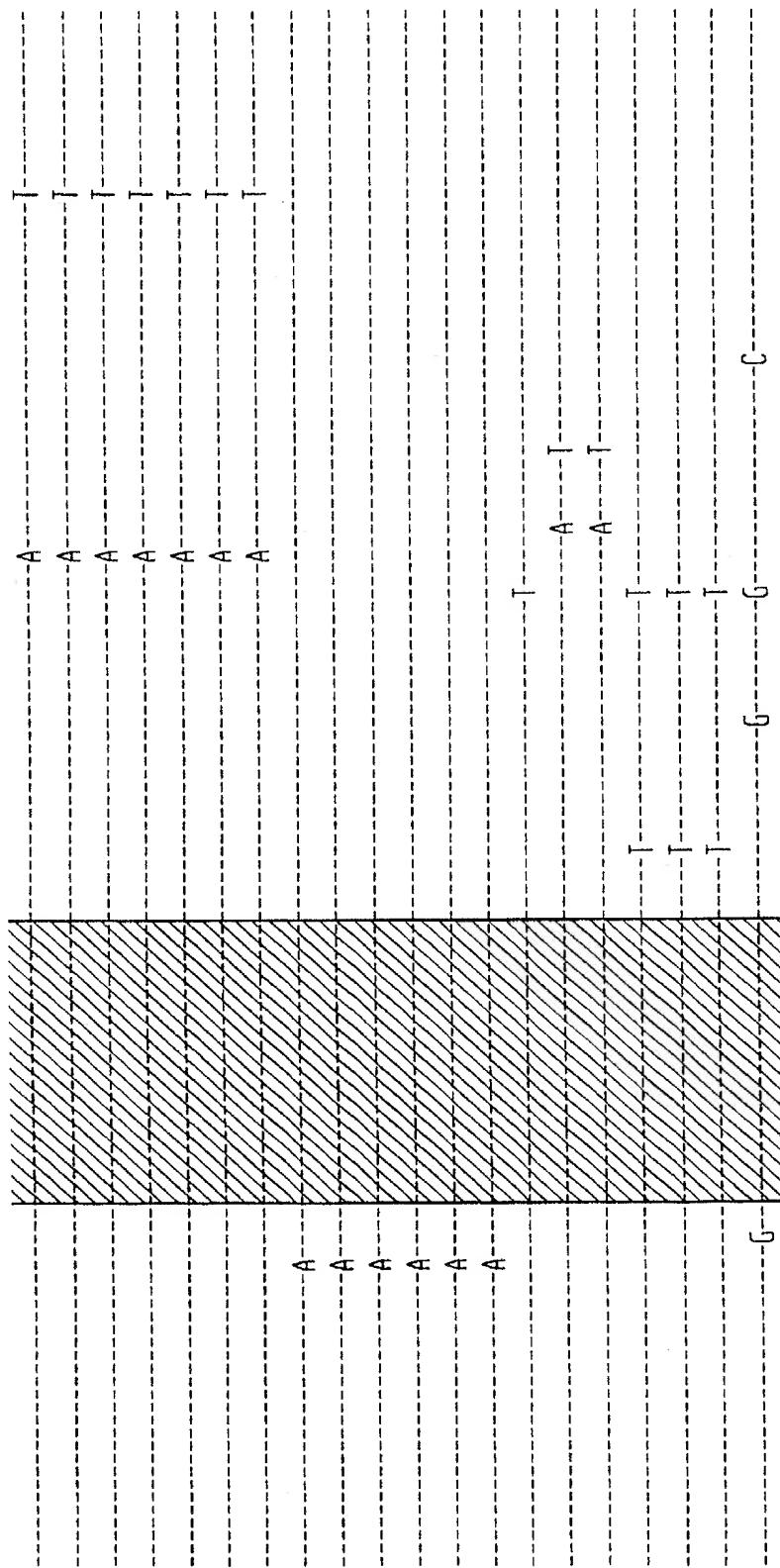


FIG. 5D

A*3101
A*3201
A*3301
A*3303
A*7401
A*7402
A*7403
A*2301
A*2402
A*2403
A*2404
A*2405
A*2407
A*0301
A*1101
A*1102
A*3001
A*3002
A*3004
A*8001

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HLA-A [Intron 3, Teil 1]	1	10	20	30	40	50	60	70	80	90	100	110	120
Consensus	G	T	A	C	A	G	G	C	A	C	G	G	G
A*0101	-	-	-	-	-	-	-	-	-	-	-	-	-
A*0301	-	-	-	-	-	-	-	-	-	-	-	-	-
A*1101	-	-	-	-	-	-	-	-	-	-	-	-	-
A*1102	-	-	-	-	-	-	-	-	-	-	-	-	-
A*3001	-	-	-	-	-	-	-	-	-	-	-	-	-
A*3002	-	-	-	-	-	-	-	-	-	-	-	-	-
A*3004	-	-	-	-	-	-	-	-	-	-	-	-	-
A*0201	-	-	-	-	-	-	-	-	-	-	-	-	-
A*0202	-	-	-	-	-	-	-	-	-	-	-	-	-
A*0203	-	-	-	-	-	-	-	-	-	-	-	-	-
A*0204	-	-	-	-	-	-	-	-	-	-	-	-	-
A*0205	-	-	-	-	-	-	-	-	-	-	-	-	-
A*0206	-	-	-	-	-	-	-	-	-	-	-	-	-
A*0207	-	-	-	-	-	-	-	-	-	-	-	-	-
A*0208	-	-	-	-	-	-	-	-	-	-	-	-	-
A*0209	-	-	-	-	-	-	-	-	-	-	-	-	-
A*0210	-	-	-	-	-	-	-	-	-	-	-	-	-
A*0211	-	-	-	-	-	-	-	-	-	-	-	-	-
A*0215	-	-	-	-	-	-	-	-	-	-	-	-	-
A*0217	-	-	-	-	-	-	-	-	-	-	-	-	-
A*6801	-	-	-	-	-	-	-	-	-	-	-	-	-
A*6802	-	-	-	-	-	-	-	-	-	-	-	-	-
A*6901	-	-	-	-	-	-	-	-	-	-	-	-	-

FIG. 6A

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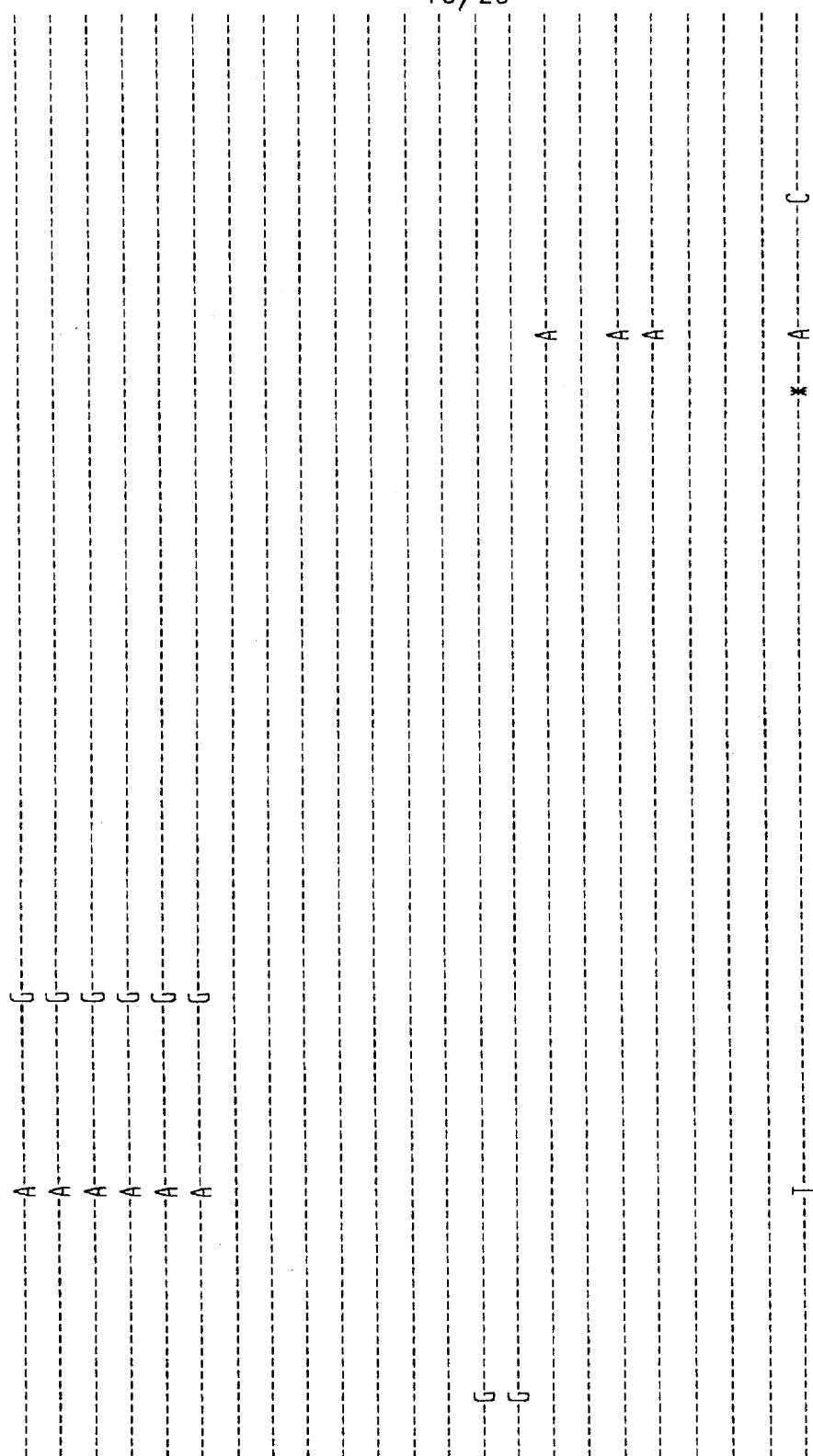


FIG. 6B

HLA-A Intron 3, Teil II

	120	140	150	160	170	180	190	200	210	220	230	240	250
Gonsensus	T	C	T	C	T	G	G	T	T	C	G	C	G
A*0101													
A*0301													
A*1101													
A*1102													
A*3001													
A*3002													
A*3004													
A*0201													
A*0202													
A*0203													
A*0204													
A*0205													
A*0206													
A*0207													
A*0208													
A*0209													
A*0210													
A*0211													
A*0215													
A*0217													
A*6801													
A*6802													

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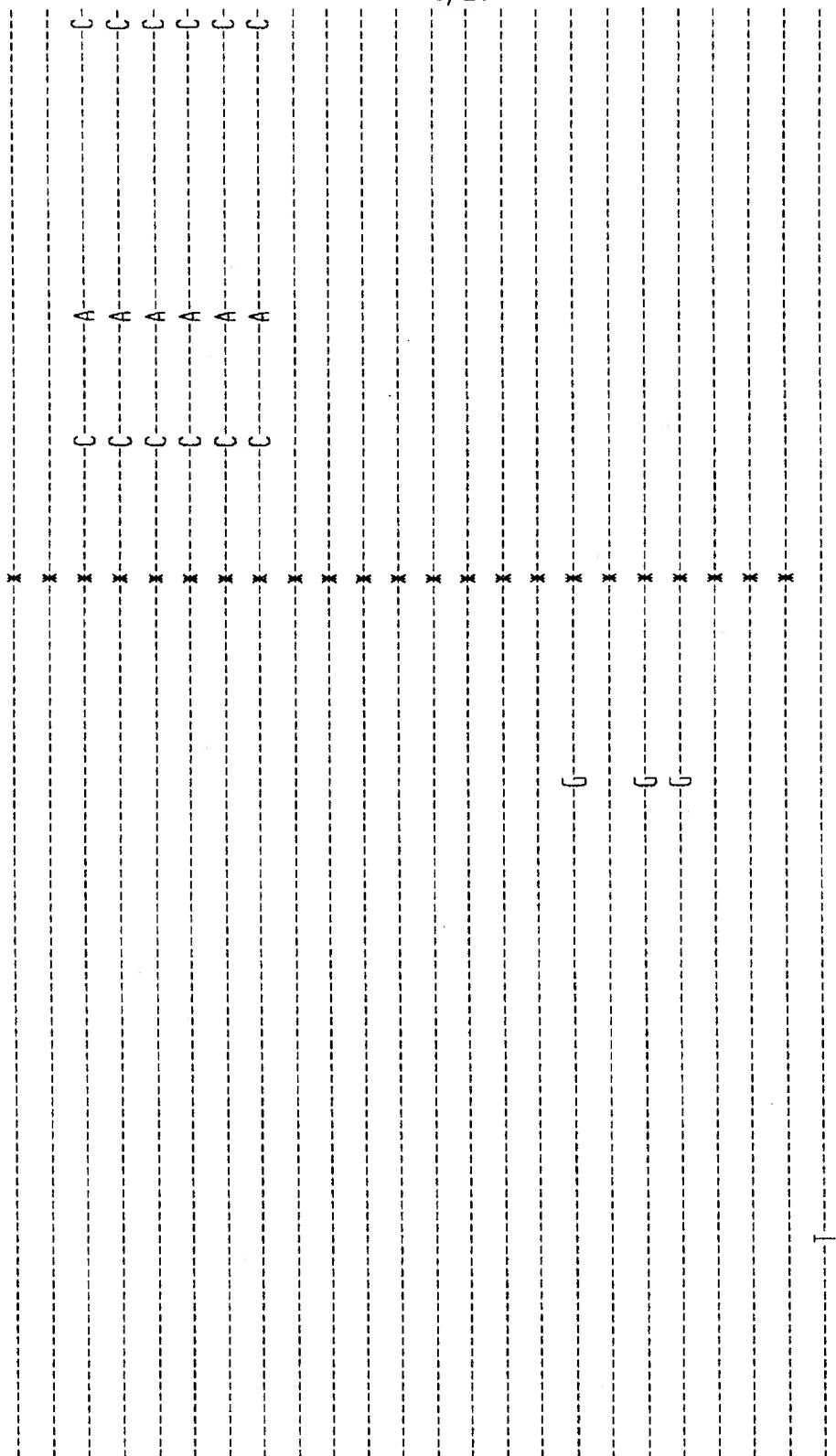


FIG.6D

A*6901

A*2301

A*2402

A*2403

A*2404

A*2405

A*2407

A*2501

A*2601

A*3402

A*4301

A*6601

A*6602

A*6603

A*2901

A*2902

A*3101

A*3201

A*3301

A*3303

A*7401

A*7402

A*7403

A*8001

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Consensus	260	270	280	290	300	310	320	330	340	350	360	370	380
A*0101	GGTTCCCTTGTACACACGGAGCCCTGGGGGGGACTTTCCCTAGGCCCTGCTCTGCTGAGCTCAGCTCTAGGCCCT												
A*0201	XXXX												
A*1101	XXXX												
A*1102	XXXX												
A*3001	XXXX												
A*3002	XXXX												
A*3004	XXXX												
A*0201													
A*0202													
A*0203													
A*0204													
A*0205													
A*0206													
A*0207													
A*0208													
A*0209													
A*0210													
A*0211													
A*0215													
A*0217													
A*6801													
A*6802													
A*6901													

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FIG. 6F

A*2301	A*2402	A*2403	A*2404	A*2405	A*2407	A*2501	A*2601	A*3402	A*4301	A*6601	A*6602	A*6603	A*2901	A*2902	A*3101	A*3201	A*3301	A*3303	A*7401	A*7402	A*7403	A*8001
--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------

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HLA-A Intron 3, Teil IV

Consensus	390	400	410	420	430	440	450	460	470	480	490	500
A*0101	ACCTAGGTAGGACCAAGTCGGCTGGCTTCCTCTTCCAGGGACTAGAAATTTCACGGATATGGAGAATTCAGGTTATCCAGGTGGCTGGTCTGCTGCTCCATCCCA	T										
A*0301		T										
A*1101		T										
A*1102		T										
A*3001		T										
A*3002		T										
A*3004		T										
A*0201												
A*0202												
A*0203												
A*0204												
A*0205												
A*0206												
A*0207												
A*0208												
A*0209												
A*0210												
A*0211												
A*0215												
A*0217												
A*6801												

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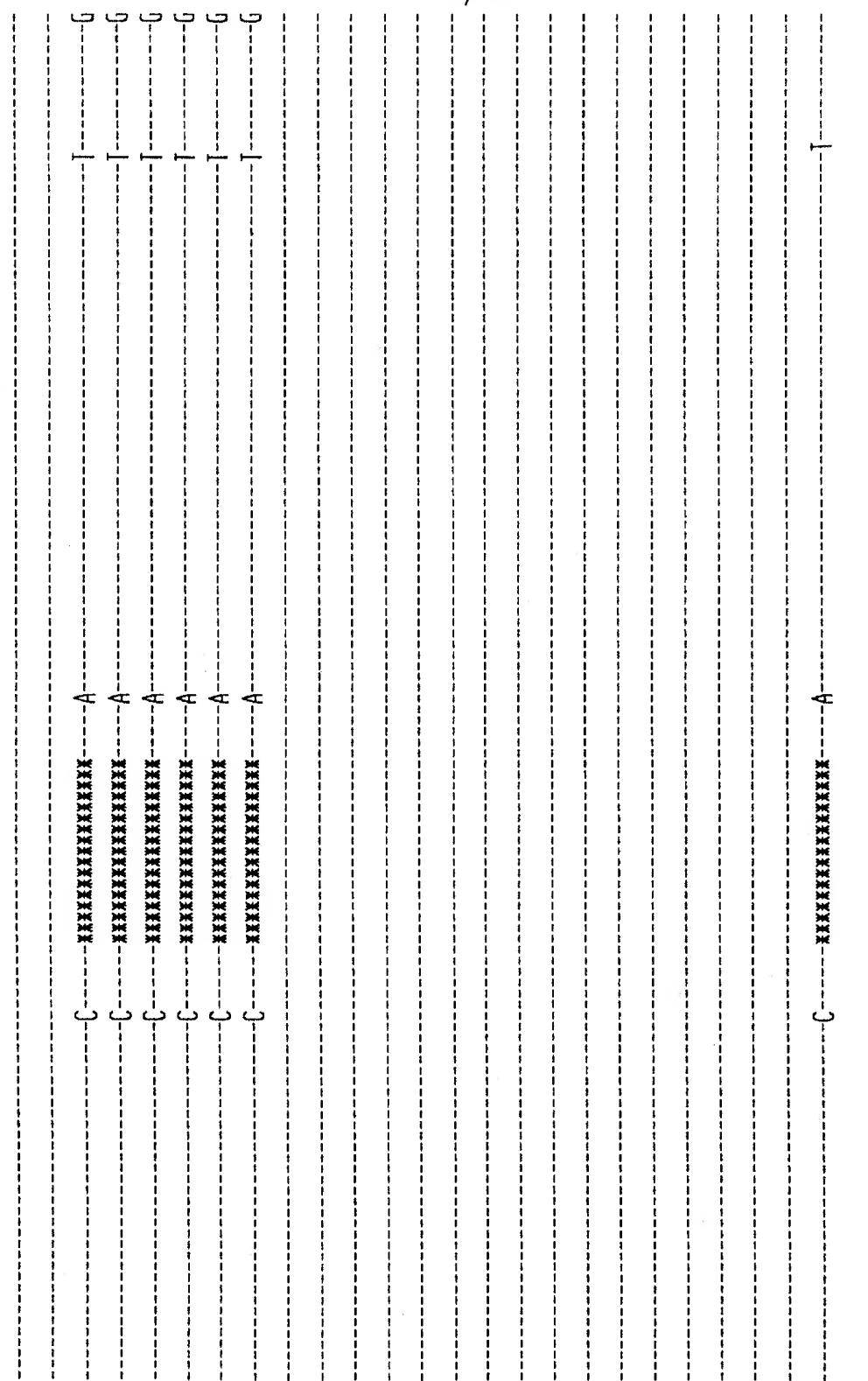


FIG. 6H

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HLA-A Intron 3, Teil V	510	520	530	540	550	560	570	580	590	600
Consensus	GGTGCCGTCATTCACATAGCCACATAGVGTGCTGGAGGTGCCATGACAGAAATGCCATGACATGACCTGACAG									
A*0101		G	C	T						C-T
A*0301		G	C	T						C-T
A*1101		G	C	T						C-T
A*1102		G	C	T						C-T
A*3001		G	C	T						C-T
A*3002		G	C	T						C-T
A*3004		G	C	T						C-T
A*0201									A	
A*0202									A	
A*0203									A	
A*0204									A	
A*0205									A	
A*0206									A	
A*0207									A	
A*0208									A	
A*0209									A	
A*0210									A	
A*0211									A	
A*0215									A	
A*0217									A	

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FIG. 6J

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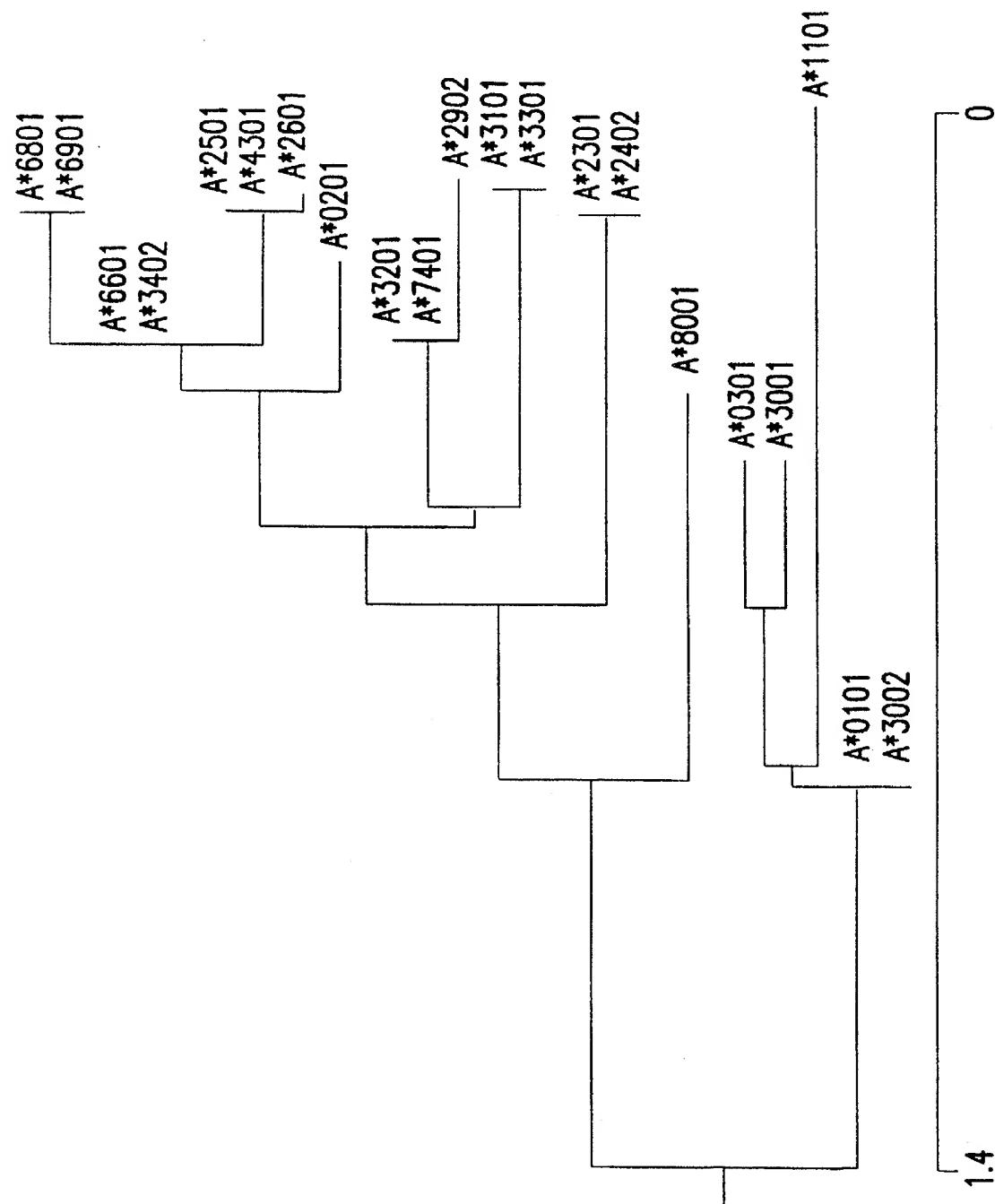
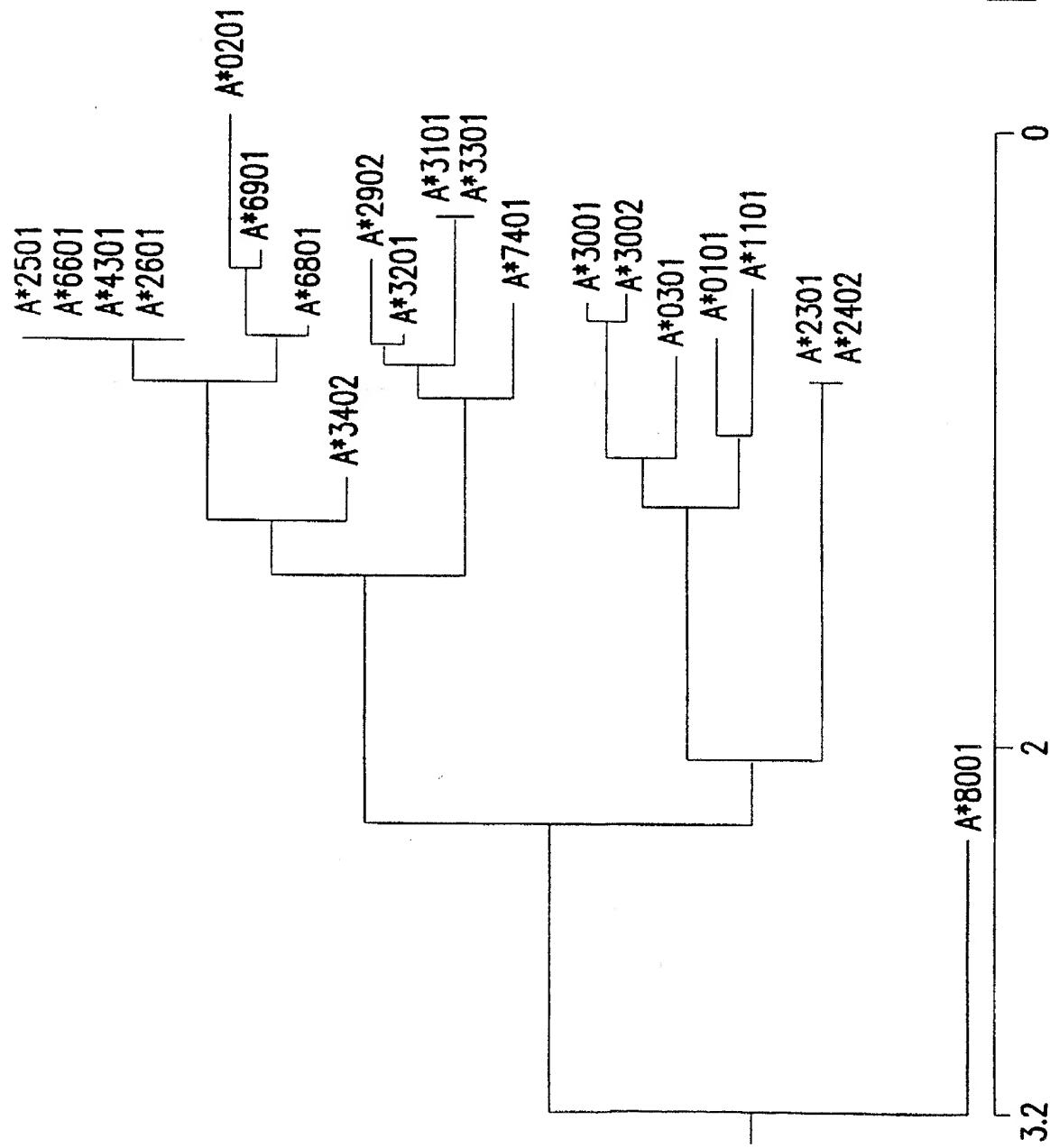


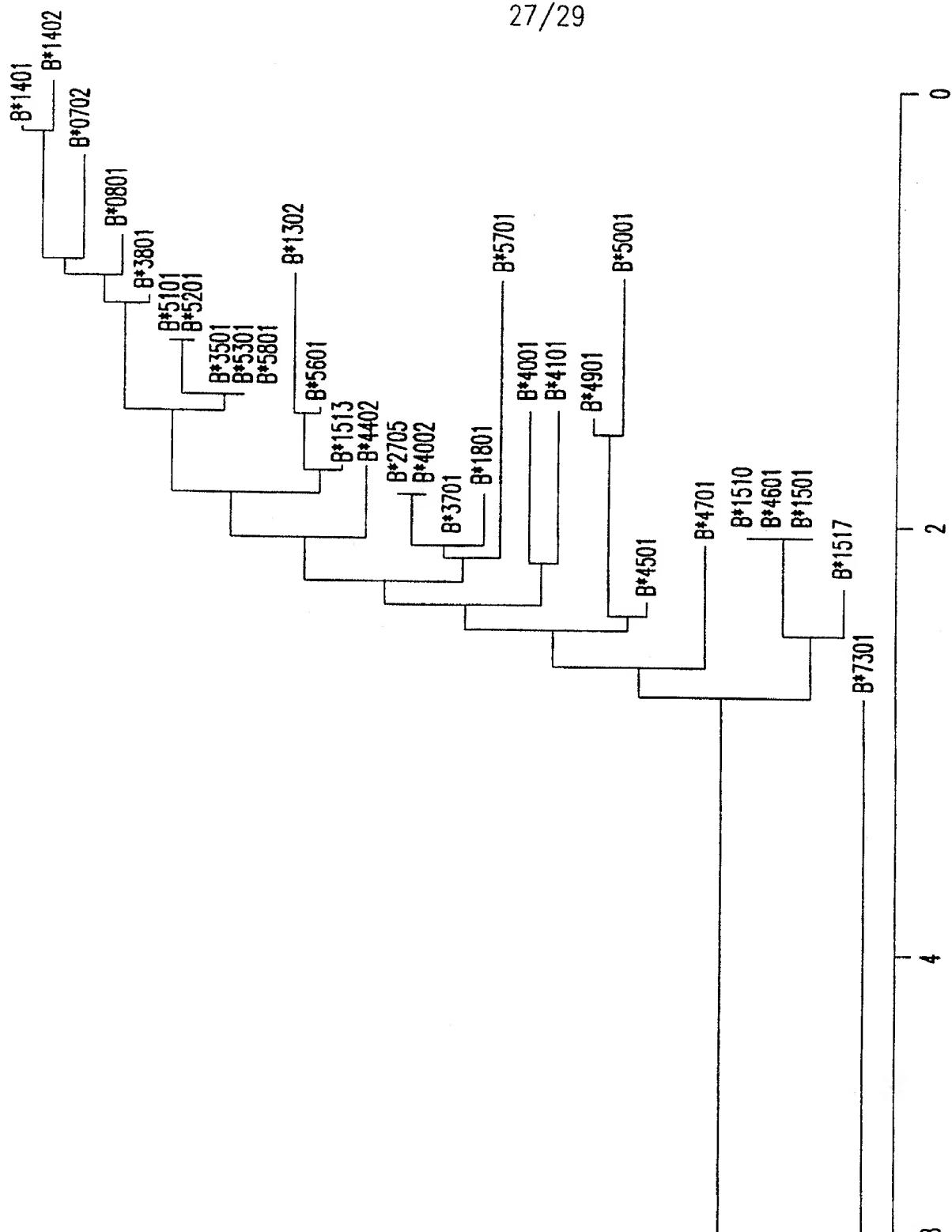
FIG. 7

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FIG.8



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16.9

8

4

2

0

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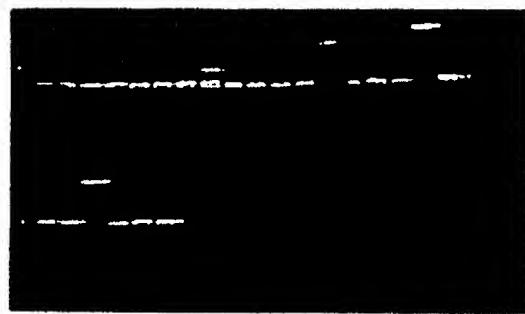


FIG.10

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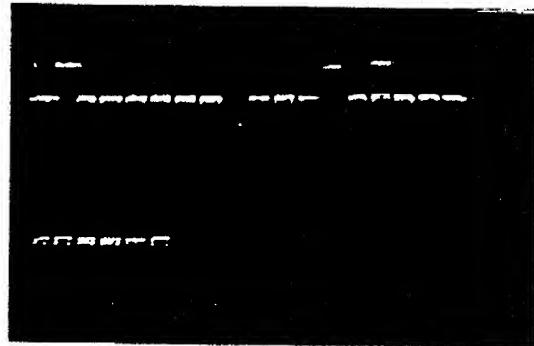
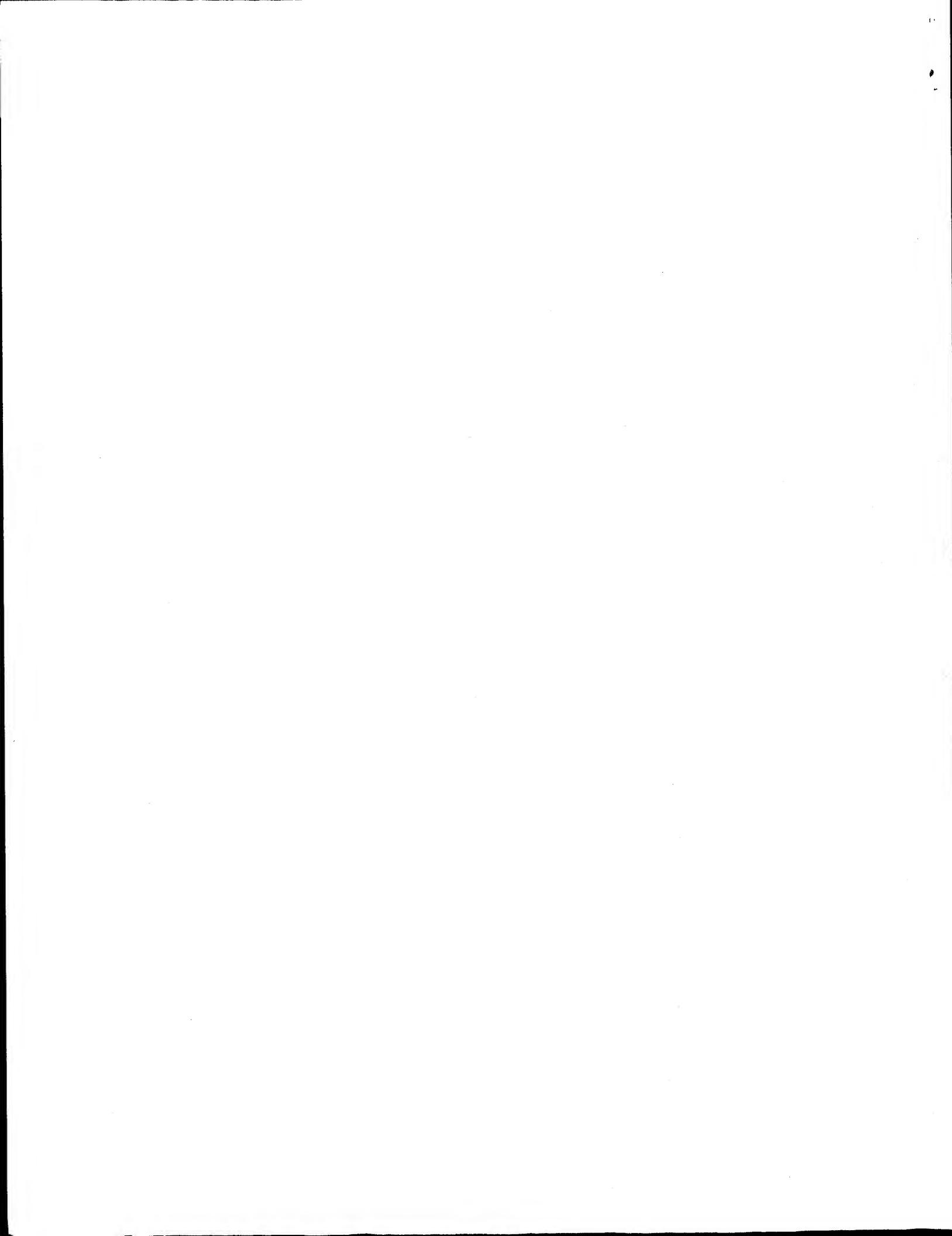


FIG.11

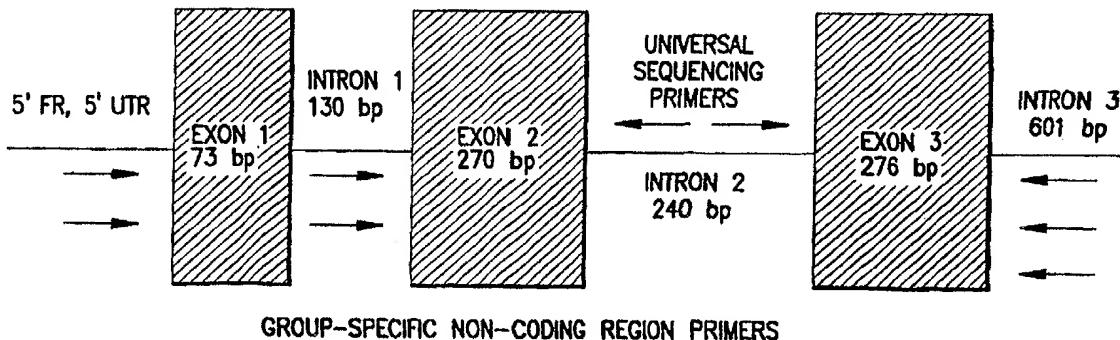




INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

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			(43) International Publication Date: 18 June 1998 (18.06.98)
(21) International Application Number: PCT/CA97/00955		(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).	
(22) International Filing Date: 12 December 1997 (12.12.97)			
(30) Priority Data: 08/766,189 12 December 1996 (12.12.96) US			
(71) Applicant (for all designated States except US): VISIBLE GENETICS, INC. [CA/CA]; Suite 1000, 700 Bay Street, Toronto, Ontario M5G 1Z6 (CA).			
(71)(72) Applicant and Inventor: BLASZCZYK, Rainer, H. [DE/DE]; Braschzeile 32, D-14109 Berlin (DE).		Published <i>With international search report.</i> <i>Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i>	
(72) Inventor; and			
(75) Inventor/Applicant (for US only): LEUSHNER, James [CA/CA]; 84 Sylvan Valley Way, North York, Ontario M5M 4M3 (CA).			
(74) Agents: STRATTON, Robert, P. et al.; Gowling, Strathy & Henderson, Suite 4900, Commerce Court West, Toronto, Ontario M5L 1J3 (CA).			

(54) Title: METHOD AND KIT FOR HLA CLASS I TYPING



(57) Abstract

The present invention relates to methods and materials for determining the HLA Class I type of a subject, wherein group-specific sequences are used to design primer molecules which may be used in amplification protocols which accurately identify the HLA group(s) and/or allele(s) carried by the subject.

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INTERNATIONAL SEARCH REPORT

International Application No

PCT/CA 97/00955

A. CLASSIFICATION OF SUBJECT MATTER
IPC 6 C12Q1/68

According to International Patent Classification(IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 6 C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category [*]	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	EP 0 414 469 A (GENETYPE AG) 27 February 1991 CLAIM 29, PAGE 49 see the whole document ----	1-25
Y	CEREB N ET AL: "LOCUS-SPECIFIC AMPLIFICATION OF HLA CLASS I GENES FROM GENOMIC DNA: LOCUS-SPECIFIC SEQUENCES IN THE FIRST AND THIRD INTRONS OF HLA-A, -B, AND -C ALLELES" TISSUE ANTIGENS, vol. 45, 1995, pages 1-11, XP000197333 see the whole document ----	1-26 -/-

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Date of the actual completion of the international search

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Date of mailing of the international search report

20/07/1998

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Y	BLASZCZYK R ET AL: "COMPLETE SUBTYPING OF THE HLA-A LOCUS BY SEQUENCE-SPECIFIC AMPLIFICATION FOLLOWED BY DIRECT SEQUENCING OR SINGLE-STRAND CONFORMATION POLYMORPHISM ANALYSIS" TISSUE ANTIGENS, vol. 46, no. 2, 1 August 1995, pages 86-95, XP000573581 see the whole document ---	1-26
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Y	CEREB ET AL.: "NUCLEOTIDE SEQUENCES OF MHC CLASS I INTRONS 1,2, AND 3 IN HUMANS AND INTRON 2 IN NONHUMAN PRIMATES" TISSUE ANTIGENS, vol. 47, no. 6, June 1996, pages 498-511, XP002070446 see the whole document & CEREB ET AL.: "ERRATUM" TISSUE ANTIGENS, vol. 48, no. 3, September 1996, pages 235-236, see the whole document ---	1-26
Y	KRAUSA P ET AL: "GENETIC POLYMORPHISM WITHIN HLA-A*02: SIGNIFICANT ALLELIC VARIATION REVEALED IN DIFFERENT POPULATIONS" TISSUE ANTIGENS, vol. 45, no. 4, 1 April 1995, pages 223-231, XP000573595 see the whole document ---	1-26
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Y	US 5 451 512 A (APPLE RAYMOND J ET AL) 19 September 1995 SEQ. 10, 15, 16, 26, 28, 29, 31, 37 see the whole document ---	1-26
		-/-

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International Application No

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Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	EP 0 540 997 A (HOFFMANN LA ROCHE) 12 May 1993 DISCLOSURE, PAGE 7 see the whole document ---	1-26
Y	WO 92 19771 A (UNIV MINNESOTA) 12 November 1992 CLAIM 9, PAGE 47 AND EXAMPLE 1, COLUMN 13-14 see the whole document ---	1-26
Y	US 5 424 184 A (SANTAMARIA PEDRO ET AL) 13 June 1995 SEQ. 1 see the whole document ---	1-26
Y	WO 95 33855 A (LUDWIG INST CANCER RES) 14 December 1995 EXAMPLE 9; PAGE 12 see the whole document ---	1-26
P,Y	CEREB ET AL.: "LOCUS-SPECIFIC CONSERVATION OF THE HLA CLASS I INTRONS BY INTRA-LOCUS HOMOGENIZATION" IMMUNOGENETICS, vol. 47, 1997, pages 30-36, XP002070447 see the whole document ---	1-26
P,Y	CEREB ET AL.: "DIMORPHIC PRIMERS DERIVED FROM INTRON 1 FOR USE IN THE MOLECULAR TYPING OF HLA-B ALLELES" TISSUE ANTIGENS , vol. 50, 1997, pages 74-76, XP002070448 see the whole document ---	1-26
P,Y	WO 97 31017 A (LUDWIG INST CANCER RES) 28 August 1997 EXAMPLE 9, PAGE 13 AND PAGE 15 see the whole document ---	1-26
P,Y	WO 97 23645 A (SLOAN KETTERING INST CANCER) 3 July 1997 DISCLOSURE, PAGE 10; CLAIM 13, PAGE 7; CLAIM 16, PAGE 17 see the whole document ---	1-26
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	-/-	

INTERNATIONAL SEARCH REPORT

International Application No

PCT/CA 97/00955

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P, Y	WO 97 41259 A (LACROIX JEAN MICHEL ;HUI MAY (CA); DUNN JAMES M (CA); LEUSHNER JAM) 6 November 1997 EXAMPLE 6, PAGE 23 see the whole document ----	1-26
P, Y	WO 97 31126 A (PERKIN ELMER CORP) 28 August 1997 CLAIM 5, PAGE 56; CLAIM 10, PAGE 57; CLAIM 11, PAGE 58; CLAIM 18, PAGE 59 see the whole document ----	1-26
P, X	KOTSCHE ET AL.: "SEQUENCING OF HLA CLASS I GENES BASED ON THE CONSERVED DIVERSITY OF THE NONCODING REGIONS: SEQUENCING-BASED TYPING OF THE HLA-A GENE" TISSUE ANTIGENS, vol. 50, no. 2, August 1997, pages 178-191, XP002070449 see the whole document ----	1-26

INTERNATIONAL SEARCH REPORT

Information on patent family members

1. International Application No

PCT/CA 97/00955

Patent document cited in search report		Publication date	Patent family member(s)		Publication date
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			DE	69029018 T	22-05-1997
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